408 144 144 373

40.09 40.09 125.34 42.75

142.05 129.26 129.26 120.37 128.76

83.00 82.50 82.50 82.50 82.00

```
which shares sequence is come autoning moves manue proteins. Galanins are biologically active peptides that are present in the central and peripheral nervous system and are upregulated after spinal injury and in response to cestrogen. NHP is useful for diagnosis, drug screening, in response to costrogen. NHP is useful for diagnosis, drug screening, clinical trial monitoring and treatment of physiological disorders and imbalance. Galanins have been associated with for example regulating body weight, modulating behaviour, treating pain, inflammation, neuronal repair, Alzheimer's dementia, inflammatory bowel disease and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; neuroprotective; antimicrobial; antiinflammatory; analgesic; anoretic; antianoretic; therapy; novel human protein; NHP; galanin; drug screening; physiological disorder; body weight regulation; behaviour modulation; pain; inflammation; neuronal repair; Alzheimer's dementia; inflammatory bowel disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid sequence encoding a protein similar to proteins of the galanin family, useful for screening for molecules with therapeutic, diagnostic and pharmacogenic applications -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "Novel human protein (NHP) #1 which share
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                present sequence is a cDNA encoding novel human protein (NHP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= c
/product= "Mature novel human protein (NHP) #1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence similarity with galanin proteins" 1..96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Galanin family protein, novel human protein (NHP) cDNA #1.
                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAD04547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 426 BP; 107 A; 127 C; 120 G; 72 T; 0 other;
/SIDSI/gcgdata/geneseq/geneseqn/Nal999.DaT:AA200278
/SIDSI/gcgdata/geneseq/geneseqn/Na2000.DAT:AAC77994
/SIDSI/gcgdata/geneseqn/geneseqn/Na2001.DAT:AAH33498
/SIDSI/gcgdata/geneseq/geneseqn/Na2000.DAT:AAA64660
/SIDSI/gcgdata/geneseq/geneseqn/Na2000.DAT:AAA6460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilbun E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 25; 29pp; English.
                                                                                                                                                                                                                                                                                                             BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (LEXI-) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                             AAD04547 standard; cDNA; 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99US-0158848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10-OCT-2000; 2000WO-US27922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                                                                17-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97..423
/*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality: 734.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Turner CA, Donoho G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-300218/31.
                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE01017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200127273-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                L2-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                  AAD04547;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Key
                                                                                                                                                                                                                                                                                                                                                                               5441
17133
17133
2643
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             784
2200
2408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4692
4692
4692
1704
1704
5007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180
180
356
1007
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                180
567
126
98
98
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             575
                                                                                                                                                                                                                                                                          0e - 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0.0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            430.91

400.78

400.78

401.92

395.61

2211.71

2211.71

165.44

165.44

165.44

165.44

171.82

173.71

173.71

173.71

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.74

173.
                                                                                                                                                        About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 85.50
85.50
85.50
85.50
85.50
85.50
85.00
85.00
84.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sutur outly
SIDSI/gcgdata/geneseq_geneseqn_NA2001.DAT:AAD04548 +
SIDSI/gcgdata/geneseq_geneseqn_NA2001.DAT:AAD04548 +
SIDSI/gcgdata/geneseq_geneseqn_NA2001.DAT:AAD04548 +
SIDSI/gcgdata/geneseq_geneseqn_NA1999.DAT:AAZ55536 +
SIDSI/gcgdata/geneseq_geneseqn_NA1999.DAT:AAZ25536 +
SIDSI/gcgdata/geneseq_geneseqn_NA1999.DAT:AAZ25530 +
SIDSI/gcgdata/geneseq_geneseqn_NA1999.DAT:AAZ25531 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF44068 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF44068 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF44068 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF44068 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF44068 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF44066 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF25532 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF25532 +
SIDSI/gcgdata/geneseq_geneseqn_NA2010.DAT:AAF25532 +
SIDSI/gcgdata/geneseq_geneseqn_NA20101.DAT:AAF25532 +
SIDSI/gcgdata/geneseq_geneseqn_NA20101.DAT:AAF25532 +
SIDSI/gcgdata/gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /SIDSI/gcgdata/geneseq/geneseqn/NA2000_DAT:AAA64641 + /SIDSI/gcgdata/geneseq/geneseqn/NA1997_DAT:AAA64641 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAA189889 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAH15906 - /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAH15906 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAH99550 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAV04633 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAV174099 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAX86812 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAX86812 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAX86812 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAX86812 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAX86812 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAX86812 + /SIDSI/gcgdata/geneseq/geneseqn/NA2001_DAT:AAX871074 + /SIDSI/gcgdata/geneseqn/NA2001_DAT:AAX871074 + /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS1/gogdata/geneseq/geneseqn/NA2000.DAT:AAA34962 -/SIDS1/gogdata/geneseq/geneseqn/NA1993.DAT:AAQ39212 +
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS1/gcgdata/geneseq/geneseqi/Na1999.DaT:Na25527
/SIDS1/gcgdata/geneseq/geneseqi/Na2001.DaT:AaF44077
/SIDS1/gcgdata/geneseq/geneseqi/Na2001.DaT:AaF44078
/SIDS1/gcgdata/geneseq/geneseqi/Na1992.DaT:AaF48078
/SIDS1/gcgdata/geneseq/geneseqi/Na1992.DaT:AaQ28890
/SIDS1/gcgdata/geneseq/geneseqi/Na2000.DaT:AaS88387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS1/gogdata/geneseg/genesegn/NA2000.DAT:AAA34952
/SIDS1/gogdata/geneseg/genesegn/NA2000.DAT:AAF21084
                               OM of: US-09-689-911-2 to: N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZScore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database: N_Geneseq_1101:*
Database sequences: 930621
Database length: 428662619
Search time (sec): 157.690000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Strd Orig
                                                                                             Date: Mar 3, 2002 12:50 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Search information block:
                                                                                                                                                                                                                                                                Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-689-911-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length: 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       score_list:
```

Sands AT

Zambrowicz B,

141

```
Human; nootropic; neuroprotective; antimicrobial; antiinflammatory; analgesic; anoretic; antianoretic; therapy; novel human protein; NHP; galanin; drug screening; physiological disorder; body weight regulation; behaviour modulation; pain; inflammation; neuronal repair; Alzheimer's dementia; inflammatory bowel disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Novel human protein (NHP) #2 which share sequence similarity with galanin proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product= "Mature novel human protein (NHP) #2"
                                                                                                                                                                                                                            151 CAATGGTGACCAAGACGGAAAGAGGGAGACACCCTTGAGATCCTAGA 200
                                                                                                                                                                                                                                                                                                                                                                                                     84 erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                      101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
                                                                                                           Galanin family protein, novel human protein (NHP) cDNA #2.
                                                                                                                                                                   17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                       GlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAD04548
 Gaps: 0
Percent Identity: 100.000
                                                                                    from: 1 to: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 ysGluGluAspValLeuLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAD04548 standard; cDNA; 351 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           401 AGGAGGAAGATGTCCTGAAGTCA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1..351
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ω
Ratio: 5.206
Percent Similarity: 100.000
                                                                                 Align seg 1/1 to: AAD04547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= b
97..348
/*tag= c
                                      alignment_block:
US-09-689-911-2 x AAD04547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD04548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
```

```
which shares sequence similarity with galanin proteins. Galanins are biologically active peptides that are present in the central and peripheral nervous system and are upregulated after spinal injury and in response to oestrogen. Nip is useful for diagnosis, drug screening, clinical trial monitoring and treatment of physiological disorders and imbalance. Galanins have been associated with for example regulating body weight, modulating behaviour, treating pain, inflammation, neuronal repair, Alzheimer's dementia, inflammatory bowel disease and infectious
                                                                                                                                                                                                                                                   New nucleic acid sequence encoding a protein similar to proteins of the galanin family, useful for screening for molecules with therapeutic, diagnostic and pharmacogenic applications -
                                                                                                                                                                              Sands AT;
                                                                                                                                                                                                                                                                                                                                                     The present sequence is a cDNA encoding novel human protein (NHP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84 erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ....... 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                            Zambrowicz B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pLeuTrpLysAla11eAspGlyLeuProTyrSerHisProProGlnProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 CCTGTGGAAGGCCATCGATGGGCTCCCCTACTCCCACCCTCCACAGCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 1
Percent Identity: 82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 351 BP; 77 A; 115 C; 91 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                          Hilbun E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAD04548 from: 1 to: 351
                                                                                                                                                                                                                                                                                                                    Disclosure; Page 26; 29pp; English.
                                                                                                                                                                            Wang X,
                                                                                                                                            (LEXI-) LEXICON GENETICS INC
                                                                                                            99US-0158848.
                                                                            10-OCT-2000; 2000WO-US27922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               580.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-689-911-2 x AAD04548
                                                                                                                                                                          Turner CA, Donoho G,
                                                                                                                                                                                                       WPI; 2001-300218/31.
                                                                                                                                                                                                                     P-PSDB; AAE01018.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
Quality:
             WO200127273-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                                                                                                            12-OCT-1999;
                                             19-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              294
```

```
67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, sailts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of furgs acting on galanin/galanin receptor binding function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV45154 and AAZ25518 to AAX2552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                                                      Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MetalaproproSerValProLeuValLeuLeuLeuLeuLeuLeuLeuSe 17
                        .................GATCTGGGCATGCTCAGCATGAAATTCCCA 325
117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
                                                                                                                                                                                                                                                                                               function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ25536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ပ်
                                                                                                                                                                                                                              Receptor binding peptide encoding cDNA SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 473 BP; 96 A; 155 C; 124 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oqi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eg 1/1 to: AAZ25536 from: 1 to: 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 13; Page 143; 153pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohtaki T, Matsui H, Ishibashi Y,
                                                                                                                                  seq_documentation_block:
ID AAZ25536 standard; cDNA; 473 BP
                                                                                326 AGGAGGAAGATGTCCTGAAGTCA 348
                                                      134 ysGluGluAspValLeuLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                              99WO-JP01482
                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0078139
                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0266972
                                                                                                                                                                                                        21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.004
82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 580.50
Ratio: 5.004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-689-911-2 x AAZ25536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-572170/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                         WO9948920-A1
                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                  30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                             AAZ25536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align s
```

```
The present invention describes peptides (I) binding to galanin receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g. improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR3; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       333 CCAAGAGGAATGTGATGGAGACGTTTGCCAAACCAGAGATTGGA..... 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         283 CCTGTGGAAGGCCATCGATGGGCTCCCCTACTCCCACCCTCCACAGCCCT 332
                                                                         183 GGACCCTCAATAGTGCTGGCTACCTTCTGGGTCCCGTCCTCCACCTTCCC 232
83 ATGGCTCCTCCCTCCTCCTGGTCCTCCTCCTCGTCCTTGCTGAG 132
                                                                                                                                                                                                                                                         51 GlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAs 67
                                                                                                                                                                                                                                                                                                                                                                 84
                                                 17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                      34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AA225535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptides binding to galanin receptor proteins, used to,
                                                                                                                                                                                                                                                                                                                                                                 pLeuTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor binding peptide encoding cDNA SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ohtaki T, Matsui H, Ishibashi Y, Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 143; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AA225535 standard; cDNA; 695 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         134 ysGluGluAspValLeuLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             408 AGGAGGAAGATGTCCTGAAGTCA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP01482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0078139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-572170/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9948920-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus sp.
```

```
proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function requlators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAX25518 to AAX25518 to AAX45154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394 CGTTTGTCAAGCCGAGGACTGGA.....416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ......GA 418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              244 ACCICCIGGGICCIGICCICCACCITICCICAAAGGCCAACCAGGGCAGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 hrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGlu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               108 ThrProThrGlyGluGlyGluGlnGlySerGlyArgGlnSerLeuGluAs 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             8 LeuValLeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSe 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        yrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   74 yLeuProTyrSerHisProProGlnProSerLysArgAsnValMetGluT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ25530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 pLeuGlyMetLeuSerMetLysIleProLysGluGluAspValLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      419 TCTGCGCATAGTGGACAAGAATGTTCCGGATGAAGAAGCCACCCTG 464
                                                                                                                                                                                                          Sequence 695 BP; 196 A; 201 C; 143 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                   Percent Identity: 54.545
                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1 to: 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAZ25530 standard; cDNA; 974 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       417 .....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1999 (first entry)
                                                                                                                                                                   of the present invention.
                                                                                                                                                                                                                                                                                        348.50
3.747
70.455
                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AAZ25535
                                                                                                                                                                                                                                                                                                                                                                                            US-09-689-911-2 x AAZ25535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pGR2PL6 cDNA sequence.
                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                Ratio:
                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa
    88888888888%8
```

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAN45129 to AAN45154
                                                                                                                                                                                                                                                                                                     Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 GTGCTGGTTACCTCCTGGGTCCCGTACTCCATCCGCCCTCCAGGGCTGAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 CATTGATGGGCTCCCCTATCCCCAGTTCTCAGTTGGCCTCCAAGAGGAGTC 290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 191 GGAGGCGGGAAGGCGAAGACACCCTCGGGATCCTGGACCTGTGGAAGGC 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 alMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLys.Hi 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 291 TGGGGGAGACTTTCGCCAAACCAGACTCTGGA......GTAACA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         104 sArgArgGluThrProThr.GlyGluGlyGluGlnGlySerGlyArgGln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            329 ITTGTTGGAGTTCCTGACGTGGTGCCGTGGAAACGAATCCGACCAGGAAC 378
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71 alleAspGlyLeuProTyrSerHisProProGlnProSerLysArgAsnV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   38 erAlaGlyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 SerValProLeuValLeuLeuLeuValLeuLeuLeuSerLeuAlaGluTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       55 GlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAl
                                                                                                                                                                                                          Ogi K, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 974 BP; 258 A; 278 C; 229 G; 209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 140
Gaps: 5
Percent Identity: 57.857
                                                                                                                                                                                                                                                                                                                                                          Claim 13; Page 135; 153pp; Japanese
                                                                                                                                                                                                        Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                        99WO-JP01482
                                                                                                              98JP-0078139
98JP-0266972
                                                                                                                                                                     (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                342.00
3.320
73.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAZ25530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-689-911-2 x AAZ25530
                                                                                                                                                                                                                                            WPI; 1999-572170/48
                                                                                                                                                                                                                                                                                                                           kidney functioning
                                                                                                                                                                                                                                                              P-PSDB; AAY45143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
WO9948920-A1
                                                                        24-MAR-1999;
                                                                                                                              21-SEP-1998;
                                                                                                              25-MAR-1998;
                                   30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
                                                                                                                                                                                                        Ohtaki T,
```

101 AGAGGGAGACAGCCCTTGAGATCCTAGACCTGTGGAAGGCCATCGATGGG 150

58 ysargGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGly 74

41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58

```
rhe present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAX45129 to AAX45154 and AAX25518 to AAX2552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pertides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ25534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ogi K, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor binding peptide encoding cDNA SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 180 BP; 37 A; 66 C; 47 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gabs:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11; Page 142; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohtaki T, Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                                                                                       AAZ25534 standard; cDNA; 180 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-JP01482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98JP-0078139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                          21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 332.00
                                                                                                                           136 uAspValLeuLysSer 141
                                                                                                                                                       429 AGAIGCCTIGCCGTCA 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-572170/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ney functioning
                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09948920-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25-MAR-1998;
21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                                                         AAZ25534;
```

Align seg 1/1 to: AAZ25534 from: 1 to: 180

alignment_block: US-09-689-911-2 x AAZ25534

```
physiologically active peptide having a cleaved cysteine residue at the end N-terminal, and has any of the amino acid sequences given in AAB65131. The invention includes sequences AAB65137 - AAB6513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Preparation of a new physiologically active peptide having a cleaved cysteine residue as N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF44071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding a human physiologically active protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 180 BP; 37 A; 66 C; 47 G; 30 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAF44071 from: 1 to: 180
                                                                151 crecerracreceaecerecaeaeceree 180
75 LeuProTyrSerHisProProGlnProSer 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 36; 44pp; Japanese.
                                                                                                                                                                                             seq_documentation_block:
ID AAF44071 standard; DNA; 180 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0080303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99JP-0080303.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                               23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality: 332.00
Ratio: 5.533
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-689-911-2 x AAF44071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2001-019315/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JP2000270871-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2000
                                                                                                                                                                                                                                                                                               AAF44071;
```

21 rProAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnS 38

5 SerValProLeuValLeuLeuValLeuLeuLeuSerLeuAlaGluTh 21

to: AAZ25537 from: 1 to: 356

Align seg 1/1

157 GGAGGCGGGAAGGGGAAGACCCTCGGGATCCTGGACCTGTGGAAGGC 206

55 GlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAl 71

88 alMetGluThrPheAlaLysProGluIleGly 98

71 alleAspGlyLeuProTyrSerHisProProGlnProSerLysArgAsnV 88

```
The present invention describes peptides (I) binding to galanin receptor identical (I) contain the sequence APAHRGRGG or one substantially broteins. (I) contain the sequence APAHRGRGG or one substantially broteins in the describing to rat galanin receptor proteins. Products from the pand the development of drugs acting on galanin/galanin receptor binding function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAA45129 to AAA45154 and AAZ25518 to AAZ25522 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                      rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
                                                                                                     58 ysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGly 74
                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ25537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ogi K, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 356 BP; 67 A; 104 C; 108 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 18; Page 144-145; 153pp; Japanese.
                                                                                                                                                                                                                                             151 CTCCCTACTCCCACCTCCACACCCTCC 180
                                                                                                                                                                                                              75 LeuProTyrSerHisProProGlnProSer 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAZ25537 standard; DNA; 356 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pGR2PL6 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99WO-JP01482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98JP-0078139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohtaki T, Matsui H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-572170/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO9948920-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ25537;
  41
```

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV45154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                   Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AA225531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0g1 K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 13; Page 136; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohtaki T, Matsui H, Ishibashi Y,
                                 seq_documentation_block:
ID AAZ25531 standard; cDNA; 1007 BP.
                                                                                                                                                                                                                                                                                                                                                                          99WO-JP01482.
                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0078139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LID.
                                                                                                                   21-DEC-1999 (first entry)
                                                                                                                                                   pGR2PL3 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-572170/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY45144.
                                                                                                                                                                                                                                                                                                     W09948920-A1.
                                                                                                                                                                                                                                                                                                                                                                       24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-1998;
                                                                                                                                                                                                                                                                        Sus scrofa.
                                                                                                                                                                                                                                                                                                                                        30-SEP-1999
```

Percent Identity: 69.149 Length: Gaps:

323.50 4.147 82.979

Quality: Ratio:

alignment_scores:

Percent Similarity:

alignment_block: US-09-689-911-2 x AAZ25537

22 X 88

```
Rattus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and AAZ25518 to AAZ25552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR3; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                 104 sArgArgGluThrProThr.GlyGluGlyGluGlnGlySerGlyArgGln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ...SerLeuGluAspLeuGlyMetLeuSerMetLysIleProLysGluGl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             418 TACGAGGTTTCAGATCTAGGCAAGCTCTGCAAGAAGGTTCCAAAGGAGAA 467
                                                                                                                                                                                                   alMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLys.Hi 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITGIIGGAGIICCIGACGIGGIGCCGIGGAAACGAAICCGACCAGGAAC 417
                                                                                                                                                                                                                                                                                                                             55 GlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAl 71
                                                                                                                                                                                                                                                                                                                                                                          71 alleAspGlyLeuProTyrSerHisProProGlnProSerLysArgAsnV 88
                                                                                                                                                                                                                                                                               erAlaGlyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
                                                                                                                                                                                     SerValProLeuValLeuLeuValLeuLeuLeuSerLeuAlaGluTh 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AA225533
                                   Sequence 1007 BP; 256 A; 293 C; 244 G; 214 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Receptor binding peptide encoding cDNA SEQ ID NO:39.
                                                                              Length: 140
Gaps: 57.857
                                                                                                                                                                 to: 1007
                                                                                                                                                                Align seg 1/1 to: AA225531 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
ID AAZ25533 standard; cDNA; 180 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                323.00
3.106
74.286
               of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uAspValLeuLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            #68 AGATGCCTTGTCGTCA 483
                                                                                                                               alignment_block:
US-09-689-911-2 x AAZ25531
                                                                                   Quality:
                                                                                                        Percent Similarity:
                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        W09948920-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-SEP-1999
                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ25533;
                                                                                                                                                                                                                                                                                                                                                                                                                          88
                                                                                                                                                                                                                                                                                                                                                                                                                                               331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             368
```

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAX45154 and AAZ25518 to AAZ25522 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                      Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     51 ccrccrescrecrecrecretrecreaassecaaccasses 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGly 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF44070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 58
Gaps: 0
Percent Identity: 77.586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA encoding a rat physiologically active protein.
                                                                                                                                                                                 Ogi K, Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAZ25533 from: 1 to: 180
                                                                                                                                                                                                                                                                                                                                                               Claim 11; Page 142; 153pp; Japanese
                                                                                                                                                                              Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 CTCCCTTATTCCCGCTCTCCAAGG 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75 LeuProTyrSerHisProProGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAF44070 standard; DNA; 180 BP
99WO-JP01482.
                                                   98JP-0078139
98JP-0266972
                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.673
89.655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 243.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-689-911-2 x AAZ25533
                                                                                                                                                                                 Ohtaki T, Matsui H,
                                                                                                                                                                                                                                     WPI; 1999-572170/48
                                                                                                                                                                                                                                                                                                                 kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
24-MAR-1999;
                                                      25-MAR-1998;
                                                                               21-SEP-1998;
```

```
This invention relates to a method for the preparation of a physiologically active peptide having a cleaved cysteine residue at the end N-terminal, and has any of the amino acid sequences given in AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153 which represent proteins related to the main proteins of the invention, including aplanin receptors, and basic fibroblast growth factor. DNA sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are used in the isolation and characterisation of DNA encoding the proteins of the invention.
                                                                                                                                Preparation of a new physiologically active peptide having a cleaved cysteine residue as N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bFGF (human fibroblast growth factor) DNA sequence SEQ ID 17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF44067
                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 77.586
                                                                                                                                                                                                                                                                                             Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;
                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAF44070 from: 1 to: 180
                                                                                                                                                            Disclosure; Page 35-36; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 LeuProTyrSerHisProProGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF44067 standard; DNA; 567 BP
                                           99JP-0080303
                                                              99JP-0080303
                                                                                    (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                 4.673
                                                                                                                                                                                                                                                                                                                                       243.00
                                                                                                                                                                                                                                                                                                                                                                                            US-09-689-911-2 x AAF44070
                                                                                                         WPI; 2001-019315/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                          alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                 Ratio:
JP2000270871-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP2000270871-A
                                          24-MAR-1999;
                                                              24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                     03-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF44067;
```

```
physiologically active peptide having a cleaved cysteine residue at the end N terminal, and has any of the amino acid sequences given in AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153 which represent proteins related to the main proteins of the invention, including galanin receptors, and basic fibroblast growth factor. DNA sequences AAR44065 - AAR44071 and PCR primers AAR44072 - AAR44086 are used in the isolation and characterisation of DNA encoding the proteins of the invention.
                                                                                                                                                                                                                                                           Preparation of a new physiologically active peptide having a cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bFGF (human fibroblast growth factor) DNA sequence SEQ ID 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                         This invention relates to a method for the preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 CTCCCCTAT.....CCCCAG.....TCTCAGTTGGCCTCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF44068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     58 ysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 LeuProTyrSerHisProProGlnProSerLysArgAsnValMetGluTh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 567 BP; 133 A; 154 C; 163 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 75
Gaps: 2
Percent Identity: 65.333
                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 7; 44pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183 CCCAGCATTGCCCGAGGATGGCGGC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91 rPheAlaLysProGluIleGlyGly 99
                                                                                                                                                                                                                                                                                    cysteine residue as N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                   99JP-0080303
                                                                                                     99JP-0080303
                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAF44068 standard; DNA; 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232.00
4.070
76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AAF44067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-689-911-2 x AAF44067
                                                                                                                                                                                                          WPI; 2001-019315/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                 24-MAR-1999;
                                                                                                     24-MAR-1999;
03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAF44068;
```

```
physiologically active peptide having a cleaved cysteine residue at the end N-terminal, and has any of the amino acid sequences given in AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153 including proteins related to the main proteins of the invention, including galanin receptors, and basic fibroblast growth factor. DNA sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are used in the isolation and characterisation of DNA encoding the proteins
                                                                                                                                                            Preparation of a new physiologically active peptide having a cleaved
                                                                                                                                                                                                                    This invention relates to a method for the preparation of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           151 CTCCCCTAT......CCCCAG.....TCTCAGTTGGCCTCCTG 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75 LeuProTyrSerHisProProGlnProSerLysArgAsnValMetGluTh 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25 AlabroAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ25532
                                                                                                                                                                                                                                                                                                                                     Sequence 567 BP; 133 A; 153 C; 163 G; 118 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                               Length: 75
Gaps: 2
Percent Identity: 65.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AAF44068 from: 1 to: 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine ligand (1-60) encoding cDNA.
                                                                                                                                                                                                Disclosure; Page 7; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183 TCCAGCATTGCCCGAGGATGGCGGC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91 rPheAlaLysProGluIleGlyGly 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAZ25532 standard; cDNA; 180 BP
                                                                                                                                                                           cysteine residue as N-terminal
                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
                                                                                             99JP-0080303.
                                                                       99JP-0080303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                  232.00
4.070
76.000
                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-689-911-2 x AAF44068
                                                                                                                                           WPI; 2001-019315/03
                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                  of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                           JP2000270871-A.
       Homo sapiens.
                                                                       24-MAR-1999;
                                                                                              24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                          alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
                                                  03-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XEXEXEX
```

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function requiators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV45154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptides binding to galanin receptor proteins, used to, e.g. improve
Physiologically active peptide; receptor binding; galanin receptor; GALRI; GALRZ; GALRZ; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58 ysargGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGly 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS1/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF44069
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 1
Percent Identity: 75.862
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ogi K, Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Seguence 180 BP; 30 A; 59 C; 59 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: AAZ25532 from: 1 to: 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 11; Page 138; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       151 CTCCCCTAT.....CCCCAG 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75 LeuProTyrSerHisProProGln 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seg_documentation_block:
ID AAF44069 standard; DNA; 180 BP.
                                                                                                                                                                                                                                                                                                                                                          98JP-0266972.
                                                                                                                                                                                                                                                                                                                                      98JP-0078139.
                                                                                                                                                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                       99WO-JP01482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 84.483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4.622
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-689-911-2 x AAZ25532
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohtaki T, Matsui H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-572170/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY45145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                      W09948920-A1
                                                                                                                                                                                                                                                                                       24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                        25-MAR-1998;
                                                                                                                                                                                                                                     30-SEP-1999
                                                                                                                                       Sus scrofa.
```

AAF44069;

```
This invention relates to a method for the preparation of a physiologically active peptide having a cleaved cysteine residue at the end N-terminal, and has any of the amino acid sequences given in AAB65131 - AAB65137 - AAB65137 - AAB65137 - AAB65137 - AAB65137 - AAB65137 - AAB65153 including galanin receptors, and basic fibroblast growth factor. DNA sequences AAR44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are used in the isolation and characterisation of DNA encoding the proteins
                                                                                                                                                                                                                                                                                                                                 Prebaration of a new physiologically active peptide having a cleaved cysteine residue as N-terminal \bar{\phantom{a}}
                                                                                     Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
                                                         DNA encoding a pig physiologically active protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 75.862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 180 BP; 30 A; 59 C; 59 G; 32 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAF44069 from: 1 to: 180
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 35; 44pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151 crcccrar.....ccccag 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 LeuProTyrSerHisProProGln 82
                                                                                                                                                                                                                                               99JP-0080303.
                                                                                                                                                                                                                    99JP-0080303.
                                                                                                                                                                                                                                                                         (TAKE ) TAKEDA CHEM IND LTD
                            23-MAR-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouality: 226.50
Ratio: 4.622
milarity: 84.483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-689-911-2 x AAF44069
                                                                                                                                                                                                                                                                                                     WP1; 2001-019315/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                       JP2000270871-A.
                                                                                                                                                                                                                                               24-MAR-1999;
                                                                                                                                                                                                                   24-MAR-1999;
                                                                                                                                                                                      03-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                               Sus scrofa,
```

AC068525 Homo sapiens chi

```
92.50
92.50
92.50
92.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality: 734.00
Ratio: 5.206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-689-911-2 x AX112343
                                                                                                                             seq_name: gb_pat:AX112343
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ๗
                                                                                                                                                                                                                                                                                                   nemnu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                   gb_pr:Ac018712
gb_htg:Ac020681
gb_htg:Ac087898
gb_htg:Ac074027
  gb_htg:AC068525
                                                                                                                                                                                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117
                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       201
                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          947 AF188492 Homo sapiens clone pGH 694 AF188493 Homo sapiens clone pGH 694 AF188491 Rattus norvegicus gala 974 AF188490 Sus scrofa galanin-lik 100110 AC011506 Homo sapiens chromc 164824 AC023887 Homo sapiens chromc 680 M18102 Rat galanin mRNA, complé 699 I J03624 Rat galanin (a neuropept
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC011333 Homo sapiens chromd
AC069014 Mus muscullus 11 BAC
ALS91425 Mus muscullus chromd
AC026408 Homo sapiens chromd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48 ! AL589733 Homo sapiens chromd ! AF141936 Coturnix japo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX112343 Sequence 1 from Patent
| AX112345 Sequence 3 from Patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               66256 | AC087454 Homo sapiens chromos
170537 | AC073548 Homo sapiens chromos
575 | A28025 Human preprogalanin CDN
575 | AR000787 Sequence 8 from patent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9 ! AP003795 Gallus gallus genom
! AF272146 Mus musculus transmem
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        786 ! AF141935 Coturnix coturnix japo
40850 ! AB012723 Homo sapiens gene fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! AP001633 Oryza sativa geneor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF276756 Homo sapiens chromc
AC021500 Homo sapiens chromc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AC019122 Homo sapiens chrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               i AL121944 Human DNA sequence
i AC011571 Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ! Ac024514 Homo sapiens chrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ! AF022780 Glycine max nitrate
                                                                                                                                                                   OMBGEL=frame+_pan.model_-DEV=Xlp
-Q=/Cgn2_1/USPTO_spool/USO989911/runat_02032002_201655_18764/app_query.fasta_1.199
-Q=/Cgn2_1/USPTO_spool/USO989911/runat_02032002_201655_18764/app_query.fasta_1.199
-Q=/Cgn2_1/USPTO_spool/USO989911/runat_02000_-GAPDET=4.000
-QGAPEXT=0.050 -LOOPEXT=6.000 -LOOPEXT=6.000 -QGAPDET=4.000
-QGAPEXT=0.050 -KGAPDP=10.000 -KGAPEXT=6.500 -FGAPDP=6.000
-GGAPEXT=7.000 -YGAPDP=10.000 -YGAPEXT=0.500 -DELOP=6.000
-DELEXT=7.000 -START=1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST=45 -DOCALIGA-200 -TRR_R_SCORE=PECT -TRR_MAX-100 -TRR_MIN=0
-ALIGN=15 -MODE_LOCAL -OUTFWIT-PEFS -NORM-ext -HEAPSIZE=500
-ALIGN=15 -MODE_LOCAL -OUTFWIT-PEFS -NORM-ext -HEAPSIZE=500
-MINLEN-0 -MAXLEN-200000000 -USER=USO9689911_@CGN1_1_4572
-NCPU=6 -LCPU=3 -LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=30
                                                                                          About: Results were produced by the GenCore software, version 4.5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142320
169516
184917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206248
855 !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                172705
187523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 130279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            209154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                175072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       200239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         152311
        out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ESCORE I
4.56-53
5.56-40
5.56-40
5.56-40
9.16-21
4.26-13
5.26-13
5.26-13
1.94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .7e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .14
.2e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2e+03
9e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .2e+03
.2e+03
.4e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .1e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               684.86
783.42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .4e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14.99
448.96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177.64
400.74
4.39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     985.50
                                                                                                                  Copyright (c) 1993-2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110.53
110.53
110.53
110.72
110.72
110.73
110.73
110.73
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
110.33
11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25
90
10
        OM of: US-09-689-911-2 to: GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query: US-09-689-911-2
Query length: 141
Database: GenEmbl:*
Database sequences: 1472140
Database length: -341344837
Search time (sec): 1464.4440000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  999.50
999.00
999.00
999.00
999.00
999.00
999.00
999.00
999.00
999.00
999.00
999.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       734.00
580.50
580.50
580.50
348.50
280.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            148.00
104.50
104.50
101.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strd Orig
                                                                                                                                                                                                                                                                                                                                                                                                          -NO_XLPXY -WAIT -THREADS=1
                                                Date: Mar 3, 2002 12:47 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search information block:
                                                                                                                                                        Command line parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           em_htg_hum:AC073396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    em_htg_hum:AC024514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_htg:#C087454
gb_htg:#C073548
gb_pat:#C8025
gb_pat:AR009787
gb_ov:AP003795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_pr:AC011506
gb_htg:AC023887
gb_htg:AC024580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_pr:HSDJ31316
gb_htg:AC011571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_htg:AL445199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_htg:AC073732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_pr:AC013272
gb_htg:AC092603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_htg:AF276756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_pat:AX112343
gb_pat:AX112345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gb_htg:AL589733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gb_htg:AC019122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_htg:AL591425
gb_htg:AC026408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_ov: AF141935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_ov: AF141936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gb_p1:AF022780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_ro:AF272146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_pl:AP003199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_pr:AB012723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_pl:AP001633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gb_ro:AC069014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_pr:AF188493
gb_ro:AF188491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_om:AF188490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_om:BTGALAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_ro:RATGALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gb_ro:RATGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   score_list:
```

```
AC018712 Homo sapiens BP
AC020681 Homo sapiens Cl
AC087898 Mus musculus Cl
AC074027 Mus musculus Cl
                                                                                                                                                                                                                                                                                                                                                                                                Sands, A.T.

Human galanin family proteins and polynucleotides encoding the same
Patent: WO 0127273-A 1 19-APR-2001;
                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 426)
Turner.C.A., Donoho,G., Wang,X., Hilbun,E., Zambrowicz,B. and
                                                                                                                                                                         01-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      11 CCTGGCAGAGACTCCAGCATCCGCACCTGCCCACCGGGGACGAGGAGGGCT 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 GGACCCTCAATAGTGCTGGCTACCTTCTGGGTCCCGTCCTCCACCTTCCC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 Argecrecrecerecereceresterererererereres 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetalaproproSerValProLeuValLeuLeuLeuValLeuLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pleuTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 301 GCCAGGAAACACAGAAGAGAGACACCGACAGGAGAGGGGGAACAAGGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                uaps: 0
Percent Identity: 100.000
                  156833
180192
195630
199359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
1.1e+03
2.1e+03
2.4e+03
2.5e+03
2.6e+03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AX112343 from: 1 to: 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lexicon Genetics Incorporated (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
127 c 120 q 72
                                                                                                                                                                     Sequence 1 from Patent W00127273.
  107.26
102.00
101.07
100.51
100.39
                                                                                                                                                                                                                                       AX112343.1 GI:13939104
```

```
DEFINITION
                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BASE COUNT
                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                          VERSION
KEYWORDS
                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                           Human galanin family proteins and polynucleotides encoding the same Patent: WO 0127273-A 3 19-APR-2001, Lexicon Genetics Incorporated (US) Location/Qualifiers
                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 351)
                                                                                                                                                                                                                                                                Turner, C.A., Donoho, G., Wang, X., Hilbun, E., Zambrowicz, B. and
                                                                                                             01-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAlaProProSerValProLeuValLeuLeuLeuLeuLeuLeuLeuLeu 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGGCTCCTCCGTCCCCTGGTCCTCCTCCTCGTCCTCTTGCTGAG 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pLeuTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51 GlnMetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 82.270
                                                                                                                                                                                                                                                                                                                                                                                                         ¥
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                         68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          from: 1 to: 351
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
115 c 91 g 68
                                                                                                        AX112345 351 bp DNA
Sequence 3 from Patent W00127273.
AX112345 AX112345.1 GI:13939105
134 ysGluGluAspValLeuLysSer 141
                           401 AGGAGGAAGATGTCCTGAAGTCA 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AX112345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 580.50
Ratio: 5.004
Percent Similarity: 82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-689-911-2 x AX112345
                                                            seq_name: gb_pat:AX112345
                                                                                        seq_documentation_block:
                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                     77 a
                                                                                                                                                                                                                                                                              Sands, A. T
                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                     DEFINITION
                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                       ACCESSION
                                                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29
                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          295
                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                   SOURCE
```

```
/product="galanin-like peptide precursor"
/proteln_id="AAF19724.1"
/db_xref="G1:6634714"
/tarnslation="mAPPSVPLVLLLVLLLSLAETPASAPAHRGRGGWTLNSAGYLLG
PVLHLPQWGQDGRKETALETLDLWRAIDGLPYSHPPQPSKRNVWETFAKFBIGDLGM
LSMKIRKEEDVLKS"
                                                                                                                                                                                                                                                                                        AF188492 947 bp mRNA PRI 24-DEC-1999 Homo sapiens clone pGR2HL14 galanin-like peptide precursor, mRNA, osmplete cds.
AF188492 AF188492.1 GI:6634713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
Evikaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 947)
1 (bases 1 to 947)
2 (bases 1 to 947)
2 (bases 1 to 947)
3 (bases 1 to 947)
3 (bases 1 to 947)
4 (bases 1 to 947)
5 (bases 1 to 947)
6 (bas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  183 GGACCCTCAATAGTGCTGGCTACCTTCTGGGTCCCGTCCTCCCACCTTCCC 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 1
Percent Identity: 82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1 to: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. 947
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pGR2HL14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="neuropeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 g
134 ysGluGluAspValLeuLysSer 141
                                                                                        326 AGGAGGAAGATGTCCTGAAGTCA 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ohtaki, T. and Kumano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580.50
5.004
82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AF188492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-689-911-2 x AF188492
                                                                                                                                                                            seq_name: gb_pr:AF188492
                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ซ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
```

```
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MAPPSVPLVLLLVLLLSIAETPASAPAHRGRGGWTLNSAGYLLG
PVLHLPQMGDQDGKRETALEILDLWKAIDGLPYSHPPQPSKRNVMETFAKPEIGDLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ohtari, T., Kumano, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M., Kitada, C., Kurokawa, T., Onda, H. and Fujino, M. Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens clone pGR2HL02 galanin-like peptide precursor, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (21-SER-1999) Discovery Res. Labs. 1, Takeda Chemical
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                         24-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product-"galanin-like peptide precursor"
/protein_id="ARF19725.1"
/db_xref="G1:6634716"
                                                                                                                                                                                                                             377 ......GATCTGGGCATGCTCAGCATGAAAATTCCCA 407
                                                                    84 erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLys 100
                                                                                       101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
                                                                                                                                                                                                            117 rGlyArgGlnSerLeuGluAspLeuGlyMetLeuSerMetLysIleProL 134
                 67 pLeuTrpLysAlaileAspGlyLeuProTyrSerHisProProGlnProS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
20069685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AF188493 from: 1 to: 947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="neuropeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   212 g
                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="pGR2HL02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LSMKIPKEEDVLKS"
                                                                                                                                                                                                                                                                                                                        40 AGGAGGAAGATGTCCTGAAGTCA 430
                                                                                                                                                                                                                                                                                       134 ysGluGluAspValLeuLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Kumano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF188493.1 GI:6634715
                                                                                                                                                                                                                                                                                                                                                                                                                 947 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 (bases 1 to 947)
Ohtaki, T. and Kumand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      241 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82.270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        580.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-689-911-2 x AF188493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.004
                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                             seq_name#: gb_pr:AF188493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      246
                                                                                                                                                                                                                                                                                                                                                                                                                  AF188493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF188493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
```

```
/product="galanin-like peptide precursor"
/protein_id="AAR19723.1"
/db_xref="G1:6634712"
/translation="MACSKHLVLFLTILLSLAETPDSAPAHRGRGGWTLNSAGYLLGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 694)
Ohtaki, T., Kumano, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M., Kitada, C., Kurokawa, T., Onda, H. and Fujino, M. Isolation and cDNA cloning of a novel galanin-like peptide (GALP) from porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF188491 694 bp mRNA ROD 24-DEC-1999
Rattus norvegicus galanin-like peptide precursor, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 694)
0 chtaki, T. and Kumano, S.
Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
Submitted (11-SEP-1999) Discovery Res. Labs. 300-4293, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  84 erLysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLys 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 AlaArgLysHisArgArgGluThrProThrGlyGluGlyGluGlnGlySe 117
                                                                                              133 CCTGGCAGAGACTCCAGCATCGCACCGGGGACGAGGAGGGT 182
                                                                                                                                                                        17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                    34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHisLeuPro 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="neuropeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      408 AGGAGGAAGATGTCCTGAAGTCA 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 ysGluGluAspValLeuLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF188491
AF188491.1 GI:6634711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_ro:AF188491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Norway rat.
```

```
/translation="MALTYPLIVLAVLLSIMESPASAPVHRGRGGWTLNSAGYLLGPV
LHPPSRAEGGGKGKTALGILDLWKAIDGLPYPOSQLASKRSLGETFARPDSGYTFVGV
PDVVPWKRIRPGTTRFQI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS ACOLISO6 100110 bp DNA
DDETAILING Homo sapiens chromosome 19 clone CTD-2086L14, complete sequence.
ACCESSION AC011506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91 TCCAGCCTCTGCTCCGGTCCACAGGGGCGAGGAGGAGGACCACCACAACA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        141 GIGCIGGITACCTCCTGGGTCCCGTACTCCATCCGCCTCCAGGGCTGAA 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 sargargGluThrProThr.GlyGluGlyGluGlnGlySerGlyArgGln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    329 TTTGTTGGAGTTCCTGACGTGGTGCCGTGGAAACGAATCCGACCAGGAAC 378
                                                                                                                                  /product="galanin-like peptide precursor"
/protein_id="AAR19722.1"
/db_xref="G1:6634710"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 SerValProLeuValLeuLeuLeuValLeuLeuLeuSerLeuAlaGluTh 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 alMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLys.Hi 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 ...SerLeuGluAspLeuGlyMetLeuSerWetLysIleProLysGluGl 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 TACGAGGTTTCAGATCTAGGCAAGCTCTGCAAGAACGTTCCAAAGGAGAA 428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 ACTGTCCTCTGATCGTTCTTGCAGTC...CTGCTCAGCCTGATGGAGTC 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                38 erAlaGlyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 alleAspGlyLeuProTyrSerHisProProGlnProSerLysArgAsnV 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21 rProAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnS
                                                                                                                                                                                                                                                                                                                                                                              Gaps: 5
Percent Identity: 57.857
                                                                                                                                                                                                                                                          209 t
                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AF188490 from: 1 to: 974
                                       /organism="Sus scrofa"
                                                         /db_xref="taxon:9823"
                                                                                                 /note="neuropeptide"
                                                                                                                                                                                                                                                        229 g
                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AC011506.3 GI:7630361
                                                                                                                                                                                                                                                          278 C
                                                                                                                                                                                                                                                                                                                                                                        3.320
                                                                                                                                                                                                                                                                                                                                                     342.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          136 uAspValLeuLysSer 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               429 AGATGCCTTGCCGTCA 444
                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-689-911-2 x AF188490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_pr:AC011506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                          Ratio:
                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                    source
                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
VERSION
KEYWORDS
                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
VLHLSSKANQGRKTDSALEILDLWKAIDGLPYSRSPRMTKRSMGETFVKPRTGDLRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sus scrofa
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohtaki,T., Kumano,S., Ishibashi,Y., Ogi,K., Matsui,H., Harada,M., Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.
Isolation and cDNA cloning of a novel galanin-like peptide (GALP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOGUS AF188490 974 bp mRNA MAM 24-DEC-1999 DEFINITION Sus scrofa galanin-like peptide precursor, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                     244 ACCTCCTGGGTCCTGTCCTCCACCTTTCCTCAAAGGCCAACCAGGCCAGG 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91 hrPhealaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGlu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 CGTTTGTCAAGCCGAGGACTGGA.....416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             108 ThrProThrGlyGluGlyGluGlnGlySerGlyArgGlnSerLeuGluAs 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  417 .....GA 418
                                                                                                                                                                                                                                                                                                            8 LeuValLeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSe 24
                                                                                                                                                                                                                                                                                                                                                                                          24 rAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyT 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     41 yrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGly 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74 yLeuProTyrSerHisProProGlnProSerLysArgAsnValMetGluT 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 pLeuGlyMetLeuSerMetLysIleProLysGluGluAspValLeu 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |||| ::::::::: :::::|| |||||||| :::|||| 419 TCTGCGGATAGTGGACAAATGTTCCGGATGAAGAAGCCACCCTG 464
                                                                                                                                                                                  Percent Identity: 54.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
20069685
                                             155 t
                                                                                                                                          Length:
                                                                                                                                                                 Gaps:
                                                                                                                                                                                                                                                                               from: 1 to: 694
                                         143 g
                        DKNVPDEEATLNL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and Kumano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF188490.1 GI:6634709
                                         201 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 974)
Ohtaki, T. and Kumanc
                                                                                                                                    Quality: 348.50
Ratio: 3.747
nilarity: 70.455
                                                                                                                                                                                                                                                                           Align seg 1/1 to: AF188491
                                                                                                                                                                                                             alignment_block:
US-09-689-911-2 x AF188491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
LOCUS AF188490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_om:AF188490
                                       195 a
                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF188490
                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pig.
                                     BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                     Direct Submission
Submitted (07-0CT-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                      Direct Submission
Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
On Apr 21, 2000 this sequence version replaced gi:6910529.
Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 19 clone RP11-541M19, WORKING DRAFT SEQUENCE, 8 unordered pieces.
                                                                                                                                                                                                 Observations of the 100110) The Tourist Genome Center.
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 100110)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                         www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.9% of Sequence;
Quality: Phrap Quality >=40 99.9% of Sequence;
Stanfated Total Number of Errors is 0.2.
STS Content:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 94.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AC011506 from: 1 to: 100110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="CTD-2086L14"
26449 a 23149 c 22857 g 27655 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .100110
                                                                                                     2 (bases 1 to 100110)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC023887.4 GI:9838262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  280.00
5.283
96.364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 LeuGluAspLeuGly 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          884 TTAGAGGGTAAAGGA 898
                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-689-911-2 x AC011506
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WI-11903 G21646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: gb_htg:AC023887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seg_documentation_block:
                                                                                      Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                           REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                JOURNAL
                                    REFERENCE
                                                  AUTHORS
                                                                                            JOURNAL
                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                      COMMENT
                                                                          TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGIN
```

```
Submitted (18-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MM 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is rubitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence a soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                        MO 63108, USA on Aug 17, 2000 this sequence version replaced gi:7631054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chemistry: Dye-primer ET; 82% of reads Chemistry: Dye-primer ET; 82% of reads Chemistry: Dye-terminator Big Dye; 18% of reads Assembly program: Phrap; version 0.990319 Consensus quality: 160238 bases at least Q40 Consensus quality: 161837 bases at least Q30 Consensus quality: 162813 bases at least Q20 Insert size: 170000; agarose-fp Insert size: 165317; sum-of-contigs Quality coverage: 6.34 in Q20 bases; sum-of-contigs Quality coverage: 6.34 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                              Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2092: contig of 2092 bp in length 2192: gap of unknown length 7044: contig of 4852 bp in length 7144: gap of unknown length 19499: contig of 12355 bp in length 1959: gap of unknown length 34475: contig of 14876 bp in length 34575: gap of unknown length 47285: contig of 12710 bp in length 47385: contig of 12710 bp in length 72270: contig of 24885 bp in length 72270: gap of unknown length 72270: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         72370: gap of unknown length
97221: contig of 24851 bp in length
97321: gap of unknown length
164824: contig of 67503 bp in length.
                                                                                                                                                                                                                                                                                                                           force assembly_name:Contigl0"
7145. 19499
/note="assembly_name:Contigl1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19600. .34475
/note="assembly_name:Contig12"
34576. .47285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="assembly_name:Contig9
                                                                                                                                                                                                                                                                     ----- Genome Center ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
1 (bases 1 to 164824)
Waterston, R.H.
The sequence of Homo sapiens clone
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequencing vector: plasmid; 18%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="RP11-541M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vector_side:right"
2193. .7044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /chromosome="19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone_end:T7
                                                                                      2 (bases 1 to 164824)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                  Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47386
72271
72371
97222
97322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34576
47286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                          TITLE
JOURNAL
                                                                                                                                                                   JOURNAL
                REFERENCE
                                     AUTHORS
                                                                                                    REFERENCE
                                                                                                                       AUTHORS
                                                                                                                                                                                                                                    COMMENT
```

```
Direct Submission
Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Apr 20, 2001 this sequence version replaced gi:9954666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 200603)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC024580 200603 bp DNA HTG 20-APR-200
Homo sapiens chromosome 19 clone CTD-2621117, WORKING DRAFT
SEQUENCE, 51 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                      8774 CTAGATGGCTCCCCTACTCCCACCTCCACAGCCTCCAAGAGAATGT 87794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88 lMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisA 105
                                                                                                                                                             702 others
                                                                                                                                                                                                                                                                                                                                                                                                                  7% IleAspGlyLeuProTyrSerHisProProGlnProSerLysArgAsnVa 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AC024580.4 GI:13699641
HTG: HTGS_PHASE1: HTGS_DRAFT; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                         Percent Identity: 94.545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Consensus quality: 157877 bases at least 040 Consensus quality: 174287 bases at least 030
                                                                                          vector_side::ight"
ture 97322. .164824
/note="assembly_name:Contig16"
38305 a 41699 c 42797 g 41321 t
47386. .72270
/note="assembly_name:Contig14"
                                    72371. 97221 -
/note="assembly_name:Contig15"
                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: AC023887 from: 1 to: 164824
                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                           Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center Project Name: 836654, BC801678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center clone name: CITB-E1_2621117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing of Human Chromosome 19
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: Joint Genome Institute
Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 (bases 1 to 200603)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOE Joint Genome Institute.
                                                                                clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS AC024580 200603 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87895 TTAGAGGGTAAAGGA 87909
                                                                                                                                                                                                                                                                   5.283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Summary Statistics
                                                                                                                                                                                                                                                   280.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 LeuGluAspLeuGly 126
                                                                                                                                                                                                                                                                                                                                          US-09-689-911-2 x AC023887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: gb_htg:AC024580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                   Quality:
Ratio:
                                                                                                                                                                                                                                                                                   Percent Similarity:
    misc_feature
                                        misc_feature
                                                                                                                  misc_feature
                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human.
                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOURCE
```

```
Consensus quality: 180284 bases at least Q20
Estimated insert size: 192390; agarcse-fp estimation
Estimated insert size: 195603; sum-contigs estimation
Quality coverage: 5.09 in Q20 bases; agarcse-fp estimation
Quality coverage: 5.01 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 51 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                    1144: contig of 1144 bp in length
                                                                                                                                                                 gap of unknown length contig of 1772 bp in length gap of unknown length contig of 1110 bp in length
                                                                                                                                                                                                  1110 bp in length
                                                                                                                                                                                                             gap of unknown length
contig of 1124 bp in length
                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                               gap of unknown length contig of 1031 bp in length
                                                                                                                                                                                                                                                                                                                1200 bp in length
                                                                                                                                                                                                                                                                                                                                         1704 bp in length
                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                    of 1691 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                           1443 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 1314 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bp in length
                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                           ength
                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                  unknown length
of 1392 bp in 1
                                                                                                                                                                                                                                                                                                       unknown length
                                                                                                                                                                                                                                                                                                                                                                          unknown length
                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                      length
                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                     unknown len
of 1191 bp
                                                                                                                                                                                                                                                         unknown
of 1602 b
                                                                                                                                                                                                                                              1063
                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 1079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 2432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                       of 1277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2038
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 1193
                                                                                                                                                                                                                                                of
                                                                                                                                                                                                                                                                                                                   Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of
                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                              contig
gap of
                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                              contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
contig
                                                                                                                                                                                                                                                                                                                  contig
                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contig
gap of
contig
                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     contig
                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                             gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of
                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                   gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of
                                                                                                                                                                            3016:
                                                                                                                                                                                                                       5450:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47169:
                                                                                                                                                                                                                                                                                                                                                             14042
                                                                                                                                                                                                                                                                                                                           10846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41352:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41452:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42875:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14693
                                                                                                                                                                                                                       4327
                                                                                                                                                                                                                                 5451
5551
6614
6714
                                                                                                                                                                                                                                                                                                                                     10847
                                                                                                                                                                                                                                                                                                                                                                      14043
14143
15834
                                                                                                                                                                                                                                                                                                                                                                                                                                         18668
18768
20045
                                                                                                                                                                                                                                                                                                                                                                                                       15934
17377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20145
21369
21469
                                                                                                                                                                                                                                                                                                                                                                                                                               17477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22783
22883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24912
26517
26617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32047
                                                                                                                                                                                                                                                                                                                                                             12651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24812
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44694
44794
47170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           40060
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36633
```

unknown length

gap of

```
contig of 4418 bp in length
gap of unknown length
contig of 1297 bp in length
gap of unknown length
contig of 10856 bp in length
contig of 10856 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="CalTech human BAC library D" 50919 c 51731 g 46633 t 5014 others
                                                                                                                                                                                                                                                                                                                                                                                          140107: contig of 13865 bp in length
140207: gap of unknown length
150877: contig of 10670 bp in length
150877: gap of unknown length
200603: contig of 40676
                                                                                                                                                                                                                                                                                                                                                                                                                                                8 200603; contig of 49626 bp in length.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AC024580 from: 1 to: 200603
                                                                                                                                                                                                                                                contig of 5239 bp in length
gap of unknown length
contig of 5310 bp in length
                                                                                                                                                                                                                                                                                                              of 3923 bp in length
unknown length
                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                        bp in length
                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                           of 3712 bp in length
                                                                                                                                                                              bp in length
                                                                                                                                                       in length
                                                                                                            bp in length
                                                                                                                                 bp in length
                                                                bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                               length
                                                                                                                                                                                                              length
                                                                                                                                                                                                                                                                                                      length
                                                                                                                                            Length
                                                                                                                                                                                                                                     ength
                                                                                                                                                                   ength
                                                                                                                                                                                          Length
                                ength
                                                      ength
                                                                          length
                                                                                                 ength
                                                                                                                        ength
          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                         contig of 1952 b
gap of unknown l
gap of unknown l
contig of 2728 b
gap of unknown l
contig of 3265 b
gap of unknown l
gap of unknown l
contig of 4646 b
gap of unknown l
contig of 4646 b
gap of unknown l
contig of 5329 b
                                                                                                                                                                                                                                                                                  unknown
                                                      unknown
of 1828
                                                                                                                                                                                                                                                                                                        unknown
                                                                                       3063
                                                                                                   unknown
of 1036
                                            1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone="CTD-2621117"
                                                                                                                                                                                                                                                                                gap of contig contig of
                                                                                                                                                                                                                                                                                                                  contig
 gap of
contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-689-911-2 x AC024580/rev
             48405:
50809:
                                                                            54224:
57287:
                                                                                                                                                                                                                                                                                                          93668:
                                                                                                                                                                                                                                                                                                                               97691:
                                  50909:
52196:
52296:
                                                                                                                                                                                                                                                  84346:
                                                                                                                                                                                                                                                                                  89856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .200603
                                                                                                                          59439
                                                                                                                                                                       65632
                                                                                                                                                                                68832
                                                                                                                                                                                             68932
                                                                                                                                                                                                                 73678
                                                                                                                                                                                                                              79007
                                                                                                                                     62167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 5.286
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality: 148.00
                                                                                                                                                                                                                                                                                              89857
93569
93669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46306 a
                                                                                                                                                                                                      68933
                                  50810
50910
52197
                                                                                                                                     59440
62168
62268
                                                                                                                                                                                                                              73679
                                                                                                                                                                                                                                         8006
                                                                                                    57288
                                                                                                                                                                                             68833
                                                                                                                                                                                                                                                              84347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
```

```
/t_________MEGSVILLAWLLLVATLSATLGLGMPTKEKRGWTLNSAGYLLG
/translation="MARGSVILLAWLLLVATLSATLGLGMPTKEKRGWTLNSAGYLLG
/translation="MARGSVILLAWLLLVATLGLGNPLPESNIVRTIMEFLSFLHLKE
AGALDSLPGIPLATSSEDLEQS"
a 199 c 154 g 153 t
                                                                                  Rat (strain Fisher 344) pituitary cells, cDNA to mRNA, clone pEIC.
Rattus norvegicus
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                        1 (bases 1 to 680)
Vrontakis, M.E., Peden, L.M., Duckworth, M.L. and Friesen, H.G.
Isolation and characterization of a complementary DNA (galanin)
Glone from estrogen-induced pituitary tumor messenger RNA
J. Biol. Chem. 262, 16755-16758 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               galanin; neuropeptide Y. Rat (Sprague-Dawley) hypothalamus, cDNA to mRNA, (library of R.Goodman), clones rG-[2,5].
     27-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MetAlaProProSerValProLeuValLeuLeuLeuValLeuLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rat galanin (a neuropeptide) mRNA, complete cds. 103624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length: 70
Gaps: 2
Percent Identity: 41.429
                                                                                                                                                                                                                                                            1. .680
/organism="Rattus norvegicus"
/db_xref="taxon:10116"
125. .499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: RATGALA from: 1 to: 680
                                                                                                                                                                                                                                                                                                                                                                               /protein_id="AAA41187.1"
/db_xref="G1:204239"
Rat galanin mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         mRNA
                                                                                                                                                                                                                                                                                                                                                    /note="galanin"
                                                                                                                                                                                                                                                                                                                                                                        /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        dq 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J03624.1 GI:204236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus
                                                             M18102.1 GI:204238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  104.50
2.322
64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-689-911-2 x RATGALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_documentation_block:
LOCUS RATGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          325 ACTGGAAGTG 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: gb_ro:RATGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 aLeuGluIle 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       164 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                             galanin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DEFINITION
                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                    LOCUS
                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                              JOURNAL
                                                   ACCESSION
                                                                                                                                                                               REFERENCE
                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                             SUC
                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                               TITLE
                                                                                                   SOURCE
```

ORGANISM

seq_documentation_block: seq_name: gb_ro:RATGALA

us-09-689-911-2.rge

```
/translation="MARGSVILLAWLLLVATLSATLGLGMPTKEKRGWTLNSAGYLLG
PHAIDNHRSFSDKHGLTGKRELPLEVEEGRLGSVAVPLPESNIVRTIMEFLSFLHLKE
                                                                                                                                                    Draft entry and computer-readable sequence for [1] kindly provided by L.Kaplan, 04-JAN-1988.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens chromosome 11 clone RP11-43N16 map 11, LOW-PASS SEQUENCE SAMPLING
                                                                          Kaplan, L.M., Spindel, E.R., Isselbacher, K.J. and Chin, W.W. Tissue-specific expression of the rat galanin gene Proc. Natl. Acad. Sci. U.S.A. 85, 1065-1069 (1988) 88124976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 CCTGTCAGCCACTCTGGGGCTCGGGATGCCAACAAAGGAGAAGAGGGGCT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              295 CACAGATCATTAGGGACAAGCATGGCCTCACAGGCAAGAGGGAGTTACC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 MetAlaProProSerValProLeuValLeuLeuLeuValLeuLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality: 104.50 Length: 70 Ratio: 2.322 Gaps: 2 Percent Similarity: 64.286 Percent Identity: 41.429
                                                                                                                                                                                                                                                                                                                         /note="galanin signal peptide"
                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            158 t
                                                                                                                                                                                                                                                                                                                                                               /note="galanin precursor"
                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAA41186.1"
/db_xref="G1:204237"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGALDSLPGIPLATSSEDLEQS"
                                                                                                                                                                                                                                                                                       /note="galanin mRNA"
                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 a 204 c 172 g
5 bp upstream of BamHI site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  241. .330
/note="galanin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: RATGAL from: 1
                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC087454.1 GI:12039467
                                                            (bases 1 to 699)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AC087454 66256 bp
                                                                                                                                                                                                                                                                                                           . 219
                                                                                                                                                                                                              669.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                104.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG; HTGS_PHASEO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-689-911-2 x RATGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_htg:AC087454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      345 ACTGGAAGTG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 aleuGluIle 65
                                                                                                                                                                                                                                                                                                       sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
                                                                                                                JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                 mRNA
                                                        REFERENCE
                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                        FEATURES
                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOURCE
```

```
A (Luzea, L. o. oue.20)

Barran, B., Linton, L. Nusbaum, C., Lander, E., Allen, N., Anderson, S., Camara, M., Bastien, V., Boguslavkly, L., Boukhalter, B., Brown, A., Campoplano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearriellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Hagos, B., Heaford, A., Horton, L., Hulme, M., Iliev, I., Johnson, Y., Larocaque, K., Lamazares, R., Landers, T., Lehoczky, J., Lervine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., MecBan, P., McKernan, K., McPheeters, R., Meldrim, J., Maneus, L., Mihova, T., Mengay, V., McPhort, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Polara, V., Raymond, C., Redra, R., Ries, C., Rogov, P., Roman, J., Rosetti, M., Riley, R., Schupbas, K., Schupbas, K., Schupbas, K., Schupbas, K., Stophas, S., Theodore, J., Travers, M., Travis, N., Traillo, J., Vassiliev, H., Vael, R., Vo, A., Zember, S., Schupbas, M., Stojanovic, N., Travers, M., Travis, N., Traillo, J., Vassiliev, H., Vael, R., Vo, A., Zember, L., Zimmer, A. and Zody, M., VenW. J., Young, G., Zainoun, J., Direct, Submission
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA All repeats were identified using RepeatMasker:
Sanit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RW/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low pass sequence sampling is useful for identifying clones that may be gene-rich and allows overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that the record is updated, the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 66256)
Birren, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome 11, clone RPI1-43N16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            833 1577: contig of 745 bp in length 1578 1677: gap of 100 bp 1678 2393: contin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          732: contig of 732 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 bp
f 726 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100 bp
f 716 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100 bp
of 722 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 bp
f 753 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100 bp
f 764 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100 bp f
f 737 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of 100 bp contig of 732 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            * NOTE: This record contains 79 individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site: http://www-seq.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2394 2493; gap of 100
2494 3219; contig of 7:
320 3319; gap of 100
3320 4035; contig of 7:
4036 4135; gap of 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      10: gap of 100
6574: contig of 7
4: gap of 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center clone name: 43_N_16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7411: contig of
7511: gap of 10
8243: contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4957: gap of
5710: cor
                                                                                                                                                                 (bases 1 to 66256)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: WIBR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6674:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5810:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                be preserved.
                                                   REFERENCE
                                                                                AUTHORS
                                                                                                                                 JOURNAL
                                                                                                                                                              REFERENCE
                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
```

```
36786 36885: gap of 100 bp 36886 37636: contig of 751 bp in length 37637 37736: gap of 100 bp 37737 38464: contig of 728 bp in length 38465 38564: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      29221 29320: gap of 100 bp 29321 30041: contig of 721 bp in length 30042 30141: gap of 100 bp 30142 30896: contig of 755 bp in length 30897 30996: gap of 100 bp 100 bp 30997 30996: gap of 100 bp 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34279 34378: gap of 100 bp
34379 35119: contig of 741 bp in length
35120 35219: gap of 100 bp
35220 35965: contig of 746 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p of 100 bp
contig of 715 bp in length
p of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65: gap of 100 bp
36785: contig of 720 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26744 26843: gap of 100 bp 26844 27559: contig of 716 bp in length 27560 27559: gap of 100 bp 27660 27659: gap of 100 bp in length 27660 28403: gap of 100 bp in length 28604 28503: gap of 100 bp in length 28604 29220: contig of 717 bp in length 28504 29220: contig of 717 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12580 32679: gap of 100 bp
12680 33414: contig of 735 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3415 33514: gap of 100 bp
33515 34278: contig of 764 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24240 24339: gap of 100 bp 24340 25073: contig of 734 bp in length 25074 25173: gap of 100 bp 25902 26001; gap of 100 bp in length 25902 26001; gap of 100 bp in length 25002 26743: contig of 742 bp in length 26002 26743: contig of 742 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86: gap of 100 bp 100 bp 22540: contig of 754 bp in length 23382: contig of 742 bp in length 482: gap of 100 bp 100 bp 124239: contig of 757 bp in length 24239: contig of 757 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16761: gap of 100 bp 17487: contig of 726 bp in length 17587: gap of 100 bp 17587: contig of 763 bp in length 18450: gap of 100 bp 1850: contig of 763 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14156 14255: gap of 100 bp 14256 14985: contig of 730 bp in length 14986 15085: gap of 100 bp 15831 15930: contig of 745 bp in length 15831 15930: gap of 100 bp 15831 15931 16661: contig of 731 bp in length 15931 16661: contig of 731 bp in length
                                                                                                                                                                                                                                                                                                                                              11602 11701: gap of 100 bp 11702 12439: contig of 738 bp in length 12440 12539; gap of 100 bp 12540 13299: contig of 760 bp in length 13300 13399: gap of 100 bp in length 13400 134155: contig of 756 bp in length 13400 14155: contig of 756 bp in length 13400 14155: contig of 756 bp in length
                                                                                                                                                                              34: gap of 100 pp in length 10794: contig of 760 bp in length
of 100 bp
contig of 748 bp in length
                                                                                  9191: gap of 100 bp 9934: contig of 743 bp in length
                                                                                                                                                                                                                                                                              94: gap of 100 bp
11601: contig of 707 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11765 31864; gap of 32579; cont
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18450: gap of
19171: con
                      8244 8343: gap of
8344 9091: cor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35966 36065:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21786
                                                                                                                                                                                                                                                                                  .0795 10894:
                                                                                                                                                                                                10034:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .6662
```

```
ALTECT SUBMISSION

Submitted (22-JUN-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, On Jul 26, 2001 this sequence version replaced gi:13699754.

* NOTE: This is a 'working draft' sequence. It currently are represented as runs of N. The order of the pieces is a believed to be correct as given, however the sizes of the gaps between the are based on estimates that have provided by the submittor.

* This sequence will be replaced.

* This sequence will be replaced.

* This sequence will be preserved.

* G6052 66151; gap of unknown length

* 66052 66151; gap of unknown length

* 6789 67788; gap of unknown length

* 6789 17053; contig of 102749 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 170537)
DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Consensus quality: 167142 bases at least Q40 consensus quality: 168091 bases at least Q30 consensus quality: 168171 bases at least Q20 Estimated insert size: 168000; agarose-fp estimation Estimated insert size: 168346; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens chromosome 19 clone RP11-43N16, *** SEQUENCING IN ACCRESS ***, 3 ordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 9.83 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality coverage: 9.86 in Q20 bases; agarose-fp
                                            42399 TCCTGAAGCTGGAGGACCAGGGGAACCAGAGGCAGGTGTGAGGCTGGG 42448
                                                                                              92 heAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGluThr 108
75 uProTyrSerHisProProGlnProSerLysArgAsnValMetGluThrP 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Project Name: 423205
Center clone name: RPI1-43N16
                                                                                                                              42449 GGTCACAGCCGGAGGCTGGGTCTGTGGAGAGG......
                                                                                                                                                                                                                            42481 ...GGAGGAGACCAAGTCAGGAGGGGGCAGG 42510
                                                                                                                                                                                             109 ProThrGlyGluGlyGluGlnGlySerGlyArg 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC073548.4 GI:15022024
HTG; HTGS_PHASE2; HTGS_ACTIVEFIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 170537)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
1. .170537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center Code: JGI
                                                                                                                                                                                                                                                                                                                                                                       170537 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                seq_name: gb_htg:AC073548
                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AC073548 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 estimation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             uman.
                                                                                                                                                                                                                                                                                                                                                                                            DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
```

/organism="Homo sapiens"

source

/db_xref="taxon:9606"

```
/product."galanin"
/protein_id="cAA01907.1"
/db_xxef="G1:147490"
/translation="MARGSALLIASILIAAALSASACIWSPAKEKRGWTLNSAGYLLG
PHAGNHRSFSDKNGITSKRERREPEDDMKPGSFDRSTPENNIMRTITEFLSFLHLKEA
GALDRILLDLEPAAASSEDIERS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 575)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HUMAN GALANIN, CDNA CLONES ENCODING HUMAN GALANIN AND A METHOD OF
PRODUCING HUMAN GALANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-SEP-1995
                                                                                                                                                                                                                                                                                                                                                           ||||||| ::: ||||:::|||| 48767 CTTCTGGGGACCAAGGCCAGGCCCAGGCCCAGGTC 48816
                                                                                                                                                                                                                                                                                                                                                                                                                                                     48817 AAGGCAGAAGTGGGGCTCAGGGCCTGGAGGC.....CTTGCCGGTGTCC 48860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48861 TTGAGAGCCCTTGGATGGGCACTCAGGCCCCCATGTCCCAGCAGGGCCCT 48910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||::::::::|||
|48911 AGGGAGGTAGGCATTGAGCAGAGGGCCTTTGGAGG......TGGGG 48951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        48952 TCCTGAAGCTGGAGGACCAGGCGGGAACCAGAGGCAGGTGTGAGGCTGGG 49001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 heAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGluThr 108
                                                       203 others
                                                                                                                                                                                                                                                                                                                              14 LeuLeuLeuSerLeuAlaGluThrProAlaSerAlaProAlaHisArgGl 30
                                                                                                                                                                                                                                                                                                                                                                                                                 30 yArgGlyGlyTrpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValL 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47 euHisLeuProGlnMetGly.....AspGlnAspGlyLys 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 ArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLe 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75 uProTyrSerHisProProGlnProSerLysArgAsnValMetGluThrP 92
                                                                                                                                                                                             Percent Identity: 32.432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAT
/chromosome="19"
/clone="RP11-43N16"
39169 a 47124 c 44400 g 39641 t
                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AC073548 from: 1 to: 170537
                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49002 GGTCACAGCCGGAGGCTGGGTCTGTGGAGAGG.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               49034 ...GGAGGAGGGCCAAGTCAGGAGGGGGGGGG 49063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  109 ProThrGlyGluGlyGluGlnGlySerGlyArg 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AZBUZS 575 bp DNA
Human preprogalanin cDNA sequence.
A28025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Patent: WO 9215681-A 5 17-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A28025.1 GI:1247489
                                                                                                                                                101.50
1.637
55.856
                                                                                                                                                                                                                              alignment_block:
US-09-689-911-2 x AC073548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_pat:A28025
                                                                                                                                                   Quality:
                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                     Ratio:
                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOTIPCE
```

```
Unclassified:

I (bases 1 to 575)

Evans, H. Frances and Shine, J.

France
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 221 ...........GATGACATGAAACCAGGAAGCTTTGACAGGTCCATAC 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54 AspGlnAspGly......LysArgGluThrAlaLeuGluIleLeuAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67 pLeuTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ........ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                10 LeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 41.758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT
                                                                                                                                                                                                           Percent Identity: 41.758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AR009787 from: 1 to: 575
                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCUS AR009787 575 bp DNA
DEFINITION Sequence 8 from patent US 5756460.
ACCESSION AR009787 1 GI:3968592
                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: A28025 from: 1 to: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="unknown"
a 162 c 140 g
140 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                258 CTGAAAACAATATCATGCGCACA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84 erLysArgAsnValMetGluThr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio: 1.951
Percent Similarity: 56.044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99.50
   162 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-689-911-2 x AR009787
                                                                                                                                                                                             Ratio: 1.951
Percent Similarity: 56.044
                                                                                                                                                                    99.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_pat:AR009787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS AR009787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unclassified.
                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-689-911-2 x A28025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown.
       128 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores:
                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
          BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE
```

us-09-689-911-2.rge

1982 2991 335(

```
Sequence 8, Application US/08507016
Patent No. 3756460
GENERAL INFORMATION:
APPLICANT: EVANS, HELEN F.
APPLICANT: EVANS, HOLEN F.
TITLE OF INVENTION: HUMAN GALANIN, CDNA CLONES ENCODING
TITLE OF INVENTION: HUMAN GALANIN AND A METHOD OF PRODUCING HUMAN GALANIN
NUMBER OF SEQUENCES: 10
                                               .2 + 73.50 117.67 66.40
73.50 113.25 117.04
73.50 112.04 136.83
73.50 117.67 66.40
73.50 117.67 66.40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 LeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25
                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-507-016-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             =
=
=
=
/cgn2_6/ptcdata/1/ina/5A_COMB.seq:US-08-833-485-2 + 73.5
/cgn2_6/ptcdata/1/ina/6B_COMB.seq:US-09-137-440-2 + 73.5
/cgn2_6/ptcdata/1/ina/PcrUS_COMB.seq:PCT-US91-06148A-2 +
/cgn2_6/ptcdata/1/ina/6A_COMB.seq:US-08-795-430-48 + 73.6
/cgn2_6/ptcdata/1/ina/5A_COMB.seq:US-08-247-946A-2 - 73.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 41.758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/507,016 FILING DATE: A.5-JULY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-507-016-8 from: 1 to: 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: ROTHWELL, FIGG, ERNST & KURZ 555 THIRTEENTH STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/108,733
FILING DATE: 03-58P-1993
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 06-MAR-1992
APPLICATION NUMBER: AU PK4953
FILING DATE: 06-MAR-1991
ATTORNEY, AGENT INFORMATION:
NAME: ERNST, BARBARA G.
REGISTRATION NUMBER: 30,377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (202)783-6040
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-689-911-2 x US-08-507-016-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 575 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99.50
1.951
56.044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14..385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WASHINGTON
                                                                                                                                                                                                                           seg_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D. C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
US-08-507-016-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7,78 i.)
38506
1597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ! Pat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/1/ina/bB_COMB.seq:US-08-943-731-5 + 74.50 120.58 45.72 1817
/cgn2_6/ptodata/1/ina/bB_COMB.seq:US-09-103-840A-2 + 74.50 94.77 1.38+03 20084
/cgn2_6/ptodata/1/ina/bB_COMB.seq:US-09-103-840A-2 + 74.50 36.87 6.64-05 44037
/cgn2_6/ptodata/1/ina/bB_COMB.seq:US-09-105-537-3 - 74.00 100.04 637.32 11220
/cgn2_6/ptodata/1/ina/bB_COMB.seq:US-09-320-878-19 - 74.00 86.80 3.56+03 36778
/cgn2_6/ptodata/1/ina/SA_COMB.seq:US-09-320-878-19 - 74.00 86.80 3.56+03 38506
/cgn2_6/ptodata/1/ina/SA_COMB.seq:US-08-16-316-1 + 73.50 120.00 49.31 1597 19.00022_6/ptodata/1/ina/SA_COMB.seq:US-08-36-08-2 + 73.50 117.67 66.40 1982 19.0002_6/ptodata/1/ina/SA_COMB.seq:US-08-36-08-3 + 73.50 117.67 66.40 1982 19.0002_6/ptodata/1/ina/SA_COMB.seq:US-08-36-08-3 + 73.50 117.67 66.40 1982 19.0002_6/ptodata/1/ina/SA_COMB.seq:US-08-36-08-3 + 73.50 117.67 66.40 1982 19.0002_6/ptodata/1/ina/SA_COMB.seq:US-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36-08-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10348
10366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1030
1054
1383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             700 !
11958
                                                                                                                                                                                                  Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-0=/cgn2_1/TUSPTO_spool/US05689911/runat_02032002_201656_18784/app_query.fasta_1.199
-0=/cgn2_1/TUSPTO_spool/US05689911/runat_02032002_201656_18784/app_query.fasta_1.199
-0=/cgn2_1/TUSPTO_spool/US05689911/runat_02000_-12.000
-DEJSued_Patents_NA -QFWT=fastap -SUFFIX=rni -GAPOP=12.000
-GAPOP=4.500 -OGAPEXT=0.0050 -XGAPOP-10.000 -XGAPEXT=0.500
-GAPOP=4.500 -OGAPEXT=7.000 -YGAPOP-10.000 -YGAPEXT=0.500
-DELOP=6.000 -DELEXT=7.000 -YGAPOP-10.000 -THR_SCORE=pct
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct
-TRR_MAX=100 -THR_MN-00 -ALIGN=15 -MODELOCA_OUTPMT=fs
-NORM-ext -HEAPSIZE=500 -MINIEN-0 -MAXLEN-20000000000
-USER=US09689911_aCGN1_1_70 -NCPU-6 -ICPU=3 -LONGIGG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -NO_XLDXY -WAIT -THREADS=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1654
1030
1030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4692
4692
4692
3937
2965
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.40
10.40
10.40
10.40
10.40
10.40
10.40
36.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.50 182.34
85.50 132.13
85.50 132.13
85.50 132.13
85.50 132.13
85.50 132.13
78.50 122.13
                                                                                                                       About: Results were produced by the GenCore software, version 4.5 Copyright (c) 1993-2000 Compugen Ltd.
                           out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-507-016-8
/cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-916-917-1
                           OM of: US-09-689-911-2 to: Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query length: 141
Database: Issued_Patents_NA:*
Database sequences: 351203
Database length: 113238999
Search time (sec): 75.150000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strd Orig
                                                                             Date: Mar 3, 2002 12:23 AM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Search information block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query: US-09-689-911-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          score_list:
```

```
129 CGGGCTACCTGCTGGGCCCACATGCCGTTGGCAACCACAGGTCATTCAGC 178
                                                                                                                                                                                                                                                                                               179 GACAAGAATGGCCTCACCAGCAAGCGGGAGCTGCGGCCCGAA.....220
                                                                                                                                              39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
                                                                                                                                                                                                                                               54 AspGlnAspGly.....LysArgGluThrAlaLeuGluIleLeuAs 67
                                                                                                                                                                                                                                                                                                                                                                                                      221 ......GATGACATGAAACCAGGAAGCTTTGACAGGTCCATAC 257
                                                                                                                                                                                                                                                                                                                                                 67 pLeuTrpLysAlaIleAspGlyLeuProTyrSerHisProProGlnProS 84
32 CTCCTGCTCGCCTCCTCCTCGCGCGCGCCCTTTCTGCCTCTGCGGG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Hawkins, Phillip
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBES OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSE: Pennie & Edmonds, LLP
STREET: New York
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-916-917-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows
SOFTWARE: FASTENG for Windows Version 2.0b
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/916,917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30,605
ER: 8549-0006-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/916,917
FILING DATE: 15-AUG-1997
FILING DATE: 15-AUG-1997
FILING APPLICATION DATA:
APPLICATION NUMBER: 08/672,211
FILING DATE: 27-UN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      258 CTGAAAACAATATCATGCGCACA 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET WUMBER: 8545
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-493-495
TELEFAX: 650-493-556
TELEFAX: 650-4 penvir
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 erLysArgAsnValMetGluThr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 4692 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Abrams, Samuel B
REGISTRATION NUMBER: 3(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-916-917-1
```

Ratio:

```
||| |||:::|||||:::
1879 ACCAGGGCGCGCCCTTCCTGAGGGGGGAGGAGGCCCAAGGCTTCC 1928
                                                                                                                                                                                                                                                                                                                                                                                                                         2029 CACGGTTCTTCAAGCTACAGTTCTTCTACGTGCCTGTCAAGCGGAGCCGT 2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2079 GGGACACCCCCACCAGCCCAGCCCTCTCGGAGCCAGAGGCCCCCCT 2128
                                                                                                                                                                                                                                                                                                                                       1929 ACGCTGCGTGCTCGTGGTCTTCGGCTCGGATCTCGGGGAAGGTGGT 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2129 CCCCACAGACGCCCCGAGGCACCCGGGCCCTGCAGAGCTGGGCGCCGC. 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91 ThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGl 107
                                                                                                                                                                                                                                                                                                                                                                                           45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgGl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  77 yrSer.....HisProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                                            21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 uThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-972-631-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
Percent Similarity: 53.211 Percent Identity: 32.110
                                                                                                                             Align seg 1/1 to: US-08-916-917-1 from: 1 to: 4692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 849-0005-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 27-JUN-1996
ATTORNEY ACENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25.27
                                                                                                                                                                                                                                                                                   35 hrLeuAsnSerAlaGlyTyrLeuLeu....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/972,631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2177 ....CCCCTGGGAGGAGCACCAA 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            107 uThrProThrGlyGluGlyGluGln 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
    sequence 1, Application US/08972631
    Patent No. 5856133
    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                   alignment_block:
US-09-689-911-2 x US-08-916-917-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Pennie & Edmonds
2730 Sand Hill Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415)854-3694 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 2730 Sand
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
```

```
2129 CCCCACAGACGCCCCGAGGCACCCGGGCCCTGCAGAGCTGGGCGCGCCC 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        207 GGGACAGCACCCCCACCAGCCCAGCCCTCGGAGCCAGACGCCCCCCT 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1979 CCGGGCTTACAGCAACCTGCGGCGGCTGGAGAACAACGGTCCTCTCCTCA 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1929 ACGCTGCGTGTCGTCGTCTTCGCTCGGATCTCGGGGAAGGTGGT 1978
                                                                                                                                                                                                                                                                                                                                                                          94 ThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGl 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 yrSer......HisProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 uThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgGl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                  35 hrLeuAsnSerAlaGlyTyrLeuLeu......Gly 44
                                                                                                                                                                                                                                                                                                                                                     21 ThrproalaSerAlaProala.HisArgGlyArgGly......GlyTrpf 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-972-629-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
GAPPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                      Gaps: 6
Percent Identity: 32.110
                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-972-631-1 from: 1 to: 4692
                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/972,629 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2177 ....CCCCTGGGAGGAGGACACCAA 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 uThrProThrGlyGluGlyGluGln 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
    Sequence 1, Application US/08972629
    patent No. 5859201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pennie & Edmonds
2730 Sand Hill Road
                                                                                                                                                                                                                                                                      alignment_block:
US-09-689-911-2 x US-08-972-631-1
            LENGTH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1. CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                            1.474 53.211
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                          85.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Menlo Park
STATE: California
                                                                      , TOPOLOGY: UNKNOWN MOLECULE TYPE: CDNA US-08-972-631-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                94025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET:
```

```
2129 CCCCACAGAGGCCCCGAGGCACCGGGGCCTGCAGAGCTGGGCGCCGC. 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2079 GGGACAGCACCCCACCAGCCCAGCCCTCGGAGCCAGACGCCCCCCT 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2029 CACGGIICITICAAGCIACAGIICITCIACGIGCCIGICAAGCGGAGCCGI 2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1929 ACGCTGCGTGCTCGTGCTTCGGCTCGGATCTCGGGGAAGGTGGT 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 ThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGl 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 yrser......HisProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 uThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLySArgGl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 ThrproalaSeralaProala HisArgGlyargGly......GlyTrpT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35 hrLeuAsnSerAlaGlyTyrLeuLeu......Gly 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-972-630-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip T.
APPLICANT: Hawkins, G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                          85.50 Length: 109
1.474 Gaps: 6
53.211 Percent Identity: 32.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: 0S-08-972-629-1 from: 1 to: 4692
                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2177 ....CCCCTGGGAGGAGGACCACCAA 2197
        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 uThrProThrGlyGluGlyGluGln 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
    Sequence 1, Application US/08972630
    Patent No. 5869271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Pennie & Edmonds
2730 Sand Hill Road
                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4692 base pairs
TYPE: nucleic acid
ctrandEdness: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-689-911-2 x US-08-972-629-1
                                                                                               REGISTRATION NUMBER: 25,277
REGISTRATION NUMBER: 25,277
REPERENCE/DOCKET NUMBER: 85.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
TELEFRAX: (415)854-3694
                                                                                                                                                                                                                                                                                                                   TOPOLOGY: unknown MOLECULE TYPE: CDNA US-08-972-629-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
```

```
||| |||:::||||||:::
1879 ACCAGCGCCGCCCTTCCTGAGGGGGGGGAGGAGGATCC 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1929 ACGCTGCGTGCTCGTCGCTCGCATCGGATCTCGGGAAGGTGCT 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1979 CCGGCTTACAGCAACCTGCGGCGGGTGGAAACAACCGTCCTCTCCTCA 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2129 CCCCACAGAGGCCCCGGGGCCCTGCAGAGCTGGGGCCGCGC. 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2079 GGGACAGGCACCCCACCAGCCCAGCCCTCGGAGCCAGACGCCCCCCT 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgGl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91 ThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGl 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60 uThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77 yrSer.....HisProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/1/ina/5B_COMB.seq:US-08-672-211-1
                                                                COMPUTER REALABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85.50 Length: 109
1.474 Gaps: 6
53.211 Percent Identity: 32.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-972-630-1 from: 1 to: 4692
                                                                                                                                                                                                                        CLASSITICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/672,211
FILING DATE: 27-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
REFERENCE/DCCKET NUMBER: 8549-0005-999
TELEPHONE: (415)854-3660
TELEPHONE: (415)854-3660
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARKATERISTICS:
SEQUENCE CHARKATERISTICS:
                                                                                                                                                                                       APPLICATION NUMBER: US/08/972,630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ....CCCCTGGGAGGAGCACCAA 2197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   107 uThrProThrGlyGluGlyGluGln 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-689-911-2 x US-08-972-630-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4692 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
DEDNESS: single
                California
USA
Menlo Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
Percent Similarity:
                                                        94025
                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-972-630-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH:
```

```
1929 ACGCTGCGTGTCGTGTTTCGGCTCGGATCGGATCTCGGGGAAGGTGGT 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1979 CGGGGCTTACAGCAACCTGCGGCGGCTGGAAAACAACCGTCCTCTCCTCA 2028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2029 CACGGTTCTTCAAGCTACAGTTCTTCTACGTGCCTGTCAAGCGGAGCCGT 2078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2079 GGGACAGGCACCCACCAGCCCAGCCCTCGGAGCCAGACGCCCCCCT 2128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ThrProAlaSerAlaProAla.HisArgGlyArgGly......GlyTrpT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35 hrLeuAsnSerAlaGlyTyrLeuLeu......Gly 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 ProValLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgGl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 ThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGl 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       60 uThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77 yrSer.....HisProProGlnProSerLysArgAsnValMetGlu 90
seq_documentation_block:
Sequence 1, Application US/08672211
Sequence 1, Application US/08672211
Sequence 1, Application US/08672211
Sequence 1, Application US/08672211
TITLE OF INVENTION: Cappens, Phillip T.
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.50 Length: 109
1.474 Gaps: 6
53.211 Percent Identity: 32.110
                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/672,211 FILLIG DATE: 27-JUN-1996 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to: US-08-672-211-1 from: 1 to: 4692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8549-0005-999
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                    ADDRESSEE: Pennie & Edmonds
STREET: 2730 Sand Hill Road
CITY: Menlo Park
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 85.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)854-3660
TELEFAX: (415)854-3694
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-689-911-2 x US-08-672-211-1
                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4692 base pairs
                                                                                                                                                                           NUMBER OF SEQUENCES: 1(CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
GY: unknown
                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; MOLECULE TYPE: CDNA
US-08-672-211-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                 94025
                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH:
```

```
1929 ACGCTGCGTGTCGTGGTCTTCGGCTCGGATCGGATCTCGGGGAAGGTGGT 1978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1879 ACCAGGGCGGCGCCCTTCCTGAGGGGGGGGGGGGGCCCCAAGGCTTCC 1928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21 ThrProAlaSerAlaProAla.HisArgGlyArgGly.....GlyTrpT 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 hrLeuAsnSerAlaGlyTyrLeuLeu.....Gly 44
2129 CCCCACAGACGCCCGGAGGCACCGGGCCCTGCAGAGCTGGGGGCGCCC. 2176
                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-09-225-170-1
                                                                                                                                                                                                                                                                                   APPLICANT: Stephens, Len
APPLICANT: Hawkins, Phillip Thomas
APPLICANT: Braselmann, Sylvia
TITLE OF INVENTION: G-BETA-GAMMA REGULATED
TITLE OF INVENTION: PHOSPHATIDYLINOSITOL-3' KINASE
NUMBER OF SEQUENCES: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 6
Percent Identity: 32.110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-225-170-1 from: 1 to: 4692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: Windows SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8549-0006-999
                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds, LLP
STREET: 1155 Avenue of the Americas
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/225,170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/916,917
FILING DATE: 15-AUG-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                 2177 ....CCCCTGGGAGGAGGACCCAA 2197
                                                                   107 uThrProThrGlyGluGlyGluGln 115
                                                                                                                                                                                                          seq_documentation_block:
    Sequence 1, Application US/09225170
    Paten No. 6017763
    General INFORMATION:
    APPLICANT: Stephens, Len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 85.
TELECOMMONICATION INFORMATION:
TELEPHONE: 650-493-4935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Abrams, Samuel B
REGISTRATION NUMBER: 30,605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-689-911-2 x US-09-225-170-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELERA: 650-493-5556
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 4692 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     85.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear
US-09-225-170-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10036-2811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE:
```

```
2079 GGGACAGCCCCACCAGCCCAGCCCTCGGAGCCAGACGCCCCCT 2128
                                                                                                                                                                                                                                                                                                   2129 CCCCACAGACGCCCCGAGGCACCCGGGCCCTGCAGAGCTGGGCGCCCCC. 2176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 8, Application US/08586165
Sequence 8, Application US/08586165
Sequence 8, Application US/08586165
GENERAL INFORMATION:
APPLICANT: Laufer, Edward M.
APPLICANT: Tabin, Clifford J.
APPLICANT: Tabin, Clifford J.
APPLICANT: Tabin, Clifford J.
APPLICANT: Tabin, Clifford J.
APPLICANT: APPLICANT: SAUGHOUSES: 9
CORRESPONDENCE ADDRESS:
                                      1979 CCGGGCTTACAGCAACCTGCGGGGGGGGGGAACAACCGTCCTCTCA 2028
                                                                                                               91 ThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisArgArgGl 107
                                                                                                                                                                      77 yrSer......HisProProGlnProSerLysArgAsnValMetGlu 90
                                                                                    60 uThrAlaLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProT 77
45 ProvalLeuHisLeuPro...GlnMetGlyAspGlnAspGlyLysArgGl 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-586-165-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hamilton, Brook, Smith & Reynolds, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 27.132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-586-165-8 from: 1 to: 3937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: SYSTEM: PC-DOS/MS-DS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 16-78
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps:
                                                                                                                                                                                                                                                                                                                                                                                            2177 ....ccccrgggaggagagagcaccaa 2197
                                                                                                                                                                                                                                                                                                                                                     107 uThrProThrGlyGluGlyGluGln 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: Granahan, Patricia
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: HU95:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEPAX: (617) 861-6240
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-689-911-2 x US-08-586-165-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              : 3937 base pairs
nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.602
37.984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , MOLECULE TYPE: CDNA
US-08-586-165-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
```

27 A] 150 GC	AlaHisArgGlyArgGlyTrpThrLeuAsnSerAlaGlyTyrLeuLe 43 :::
43 uG 11 200 GG	uGlyProvalLeuHisLeuProGlnMetGlyAspG 55 :: :: :: GGGGCTCCGCAGAGCCTGCTGCTGTCGTC
55 ln 234	<pre>lnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpLysAla 71</pre>
72 II 267 CC	IleAspGlyLeuProTyrSerHisProProGlnProSerLysArgAsnVa 88
88 1M :: 317 CC	1MetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLysHisA 105
105 rg 361 GA	
107 411 GG	-
110 461 CC	ThrGlyGluGlyGluGlpGlySerGlyArg 119
sed_name: /	/cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-906-360-2
seq_documenta; Sequence 2, Sequence 2, Patent No. (GENERAL INFC APPLICANT: TITLE OF IT. TITLE REFERE CURRENT PHI FILE REFERE CURRENT PHI FORMANT APPLICANT: FARLIER APPLICANT: NUMBER OF SOFTWARE: F SOFTWARE: F SOFTWARE: F SOFTWARE: DA SOFTWARE: DA SOFTWARE: DA SOFTWARE: DA SOFTWARE: DA TYPE: DN ORGANISM:	seq_documentation_block: Sequence 2, Application US/08906360 Facent No. 601341 GENERAL INFORMATION: GENERAL INFORMATION: APPLICANT: Meruelo, Daniel APPLICANT: Pampeno, Christine TITLE OF INVENTION: MAMMALIAN HUMAN FXI-T1 TITLE, REFERENCE: 8105-010 CURRENT APPLICATION NUMBER: US/08/906,360 CURRENT FILING DATE: 1996-08-05 EARLIER APPLICATION NUMBER: 60/023,173 EARLIER APPLICATION NUMBER: 60/023,173 EARLIER APPLICATION NUMBER: 50/023,173
alignment_scores:	ores: Quality: 78.00 Length: 139 Ratio: 1.322 Gaps: 7 Alarity: 42.446 Percent Identity: 26.619
alignment_block: US-09-689-911-2	ock: 11-2 x US-08-906-360-2
Align seg 1/1	/1 to: US-08-906-360-2 from: 1 to: 2965
3 Pro 987 CCG	ProProSerValProLeuValLeuLeuValLeuLeuSerLeuAl 19 :::
19 aGl	aGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThr. 35 ::: GAACTTGAATGGCACTGGCCCTGTCCACCCAGCCTTGGCAGGGATGACCG 1065

```
Align seg 1/1 to reverse of: US-08-457-273B-41 from: 1 to: 10348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9754 GCGCTCAGCAGGTGGTGACCTTGTGGACATTTCGTAAACAAGTCAGCAGC 9705
                                                                                                                                                                                                                                                                                                                                                                                        9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACCTCAAGCACAGACTGGAA 9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |||||||:::::::::||
9654 GGCCCTGCGGTCGAGCTCCTCTATCTGGTGTCTGTAGAAGTCTGTGG 9605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 ASDVALMEtGluThrPheAlaLySProGluIleGlyGlyLysAlaArgLy 103 :::::: ||| || || || ||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103 sHisArgArgGluThrProThrGlyGluGlyGluGlnGlySerGlyArgG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              53 yAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 ysalalleAspGlyLeuProTyrSerHisProProGlnProSerLysArg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                 44 GlyProValLeuHisLeu.....ProGlnMetGl 53
                                                                                                                                                                                                                                                                                                                                                  34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
                                                                                                                                                                                        16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
                                                                                                                                                                                                                                                                     28 sArgGlyArgGlyGly......33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/1/ina/6A_COMB.seq:US-08-556-419-13
                                          Percent Identity: 26.119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: L1, Xiao-Jiang
APPLICANT: L1, Xiao-Jiang
APPLICANT: L1, Shi-Hua
APPLICANT: Lanahan, Alan
APPLICANT: Lanahan, Anthony
APPLICANT: Worley, Paul
APPLICANT: Snyder, Solomon
TITLE OF INVENTION: Huntingtin-associated protein
FILE REFERENCE: 01107.52271
        Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/556,419C CURRENT FILING DATE: 1995-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                             US-09-689-911-2 x US-08-457-273B-41/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application US/08556419C; Patent No. 6093549; GENERAL INFORMATION:
                                1.393
41.791
              78.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapiens
US-08-556-419-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                 Quality:
Ratio:
                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 13
LENGTH: 10348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9449 AA 9448
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 ln 120
                                                                                                  alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
```

```
Align seg 1/1 to reverse of: US-08-556-419-13 from: 1 to: 10348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9754 GCGCTCAGCAGGTGGTGACCTTGTGGACATTTCGTAAACAAGTCAGCAGC 9705
                                                                                                                                                                                                                                                                                                                                                9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACCTCAAGCACAGACTGGAA 9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87 AsnValMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLy 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70 ysAlalleAspGlyLeuProTyrSerHisProProGlnProSerLysArg 86
                                                                                                                                                                                                                                                                                                                                                                                     44 GlyProValLeuHisLeu.....proGlnMetGl 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                        53 yAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpL 70
                                                                                                                                                                                                                                        28 sArgGlyArgGlyGly......33
                                                                                                                                                                                                                                                                                                               34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
                                                                                                                                                                 16 LeuSerLeuAlaGluThrProAlaSerAla.....proAlaHi 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-09-041-886-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Proapoptotic Peptides, Dependence TITLE OF INVENTION: Polypeptides and Methods of Use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/041,886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                        Percent Identity: 26.119
                          Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 14, Application US/09041886 Patent No. 6235872 GENERAL INFORMATION:
                                                                                alignment_block:
US-09-689-911-2 x US-08-556-419-13/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bredesen, Dale E. APPLICANT: Rabizadeh, Sharroz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 7:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                            Ratio: 1.393
Percent Similarity: 41.791
           78.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
CLASSIFICATION:
           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9449 AA 9448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ln 120
```

APPLICANT: Duyao, Mabel P.
APPLICANT: Gusella, James F.
TITLE OF INVENTION: Huntingtin DNA, Protein And Uses Thereof
NUMBER OF SEQUENCES: 25

APPLICANT: Ambrose, Christine M.

```
Align seg 1/1 to reverse of: US-09-041-886-14 from: 1 to: 10348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9754 GCGCTCAGCAGGTGGTGACCTTGTGGACATTTCGTAAACAAGTCAGCAGC 9705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACCTCAAGCACAGACTGGAA 9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||||::::::::|||
9654 GGCCCTGCGGTCGTCCTCTTATCTGGTGTCTGTAGAAGTCTGTGG 9605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9604 CGACCAGGAGAAAAGGTTCACGTCCACCTG......9574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9573 .....Crccagcrrgcccarccrgcrgar.... 9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9549 GACATGTGGGAGGATCGCCGCGACGGGCTGGTGGTGGACGCGCTGACAA 9500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |:::
9499 AGAAGCAGAGAGAGCTCCACGTGGCGATGGCGACGGGGCCCTCTGCGTG 9450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87 AsnValMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLy 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            103 SHISArgArgGluThrProThrGlyGluGlyGluGlnGlySerGlyArgG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GlyProValLeuHisLeu.....ProGlnMetGl 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                53 yAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 ysAlalleAspGlyLeuProTyrSerHisProProGlnProSerLysArg 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 26.119
                                                                         P-LJ 2626
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-689-911-2 x US-09-041-886-14/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28 sArgGlyArgGlyGly.....
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION UNDRER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ
TELECOMMUNICATION INFORMATION:
TELEFAX: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                        LENGTH: 10348 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.393
41.791
                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                 CDS
316..9748
                                                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                               AME/KEY:
                                                                                                                                                                                                                                                                                                                                  ;
US-09-041-886-14
                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9449 AA 9448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 ln 120
```

seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-246-982A-5

seq_documentation_block:
 Sequence 5, Application US/08246982A; Patent No. 5686288; GENERAL INFORMATION:

APPLICANT: MacDonald, Marcy E.

```
Align seg 1/1 to reverse of: US-08-246-982A-5 from: 1 to: 10366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9754 GCGCTCAGCAGGTGGTGACCTTGTGGACATTTCGTAAACAAGTCAGCAGC 9705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACCTCAAGCACAGACTGGAA 9655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9654 GGCCTGCGGTCGAGCTCCTCTCTATCTGGTGTCTGTAGAAGTCTGTGG 9605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ||||||||
| 9604 CGACCAGGAGAAAGGTTCACGTCCACCTG......9574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28 sArgGlyArgGlyGly.....33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 GlyProValLeuHisLeu.....ProGlnMetGl 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53 yAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70 ysAlaIleAspGlyLeuProTyrSerHisProProGlnProSerLysArg 86
                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,982A
FILING DATE: May 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps: 6
Percent Identity: 26.119
                      E: Sterne, Kessler, Goldstein & Fox 1100 New York Avenue
                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Goldstein, Jorge, A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 0609.3880002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEG ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Ke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 1.393
Percent Similarity: 41.791
                                                                                                                                                                                                                                                                                                435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            316..9748
                          STREET: 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                  U.S.A.
                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                 20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; LOCATION:
US-08-246-982A-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                COUNTRY:
```

```
Align seg 1/1 to reverse of: US-08-453-265-5 from: 1 to: 10366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
    Sequence 5, Application US/08453265
    Patent No. 5693757
    GENERAL INFORMATION:
    APPLICANT: MacDonald, Marcy E.
    APPLICANT: MacDonald, Marcy E.
    APPLICANT: MacDonald, Marcy E.
    APPLICANT: MacDonald, Marcy E.
    APPLICANT: Gusella, James F.
    APPLICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16 LeuSerLeuAlaGluThrProAlaSerAla.....ProAlaHi 28
                                                              9549 GACATGTGGGAGGATCGCCGCGACCCACCGGCTGGTGGACGCGCTGACAA 9500
                                                                                                                                                                                              103 sHisArgArgGluThrProThrGlyGluGlyGluGlnGlySerGlyArgG 120
87 AsnvalMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLy 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/1/ina/5A_COMB.seq:US-08-453-265-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 26.119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPOTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/453,265
FILING DATE: 30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEE: Sterne, Kessler, Goldstein & Fox SEE: 1100 New York Avenue Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Ludwig, Steven R.
REGISTRATION NUMBER: 36,203
REFERENCE/DOCKET NUMBER: 0609.3880003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEPHONE: (202) 371-2540
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 10366 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               30-MAY-1995
30-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-689-911-2 x US-08-453-265-5/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 1.393
Percent Similarity: 41.791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
316..9748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
US-08-453-265-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                            9449 AA 9448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                  120 ln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
```

```
9573 .....crccagcTrGcccarccrGcTGAT.....9550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111:::: 111 11 11 11 9549 GACATGGGGGGGGCTGGACGCGCTGACAA 9500
                                                                                                                                                                                                                      9654 GGCCCTGCGGTCGAGCTCCTCCTATCTGGTGTCTGTAGAAGTCTGTGG 9605
                                                                                                                                                                                                                                                                                                9604 CGACCAGGCAGAAAGGTTCACGTCCACCTG......9574
                                                                                                                                                                                                                                                                                                                                                                                                                                            87 AsnValMetGluThrPheAlaLysProGluIleGlyGlyLysAlaArgLy 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103 sHisArgArgGluThrProThrGlyGluGlyGluGlnGlySerGlyArgG 120
                                        9754 GCGCTCAGCAGGTGGTGACCTTGTGGACATTTCGTAAACAAGTCAGCAGC 9705
                                                                                                                              9704 CGGTGATATGGGCTTCCTGGGGCTGCAACCACCTCAAGCACAGACTGGAA 9655
                                                                                                                                                                                                                                                                                                                                                         70 ysAlalleAspGlyLeuProTyrSerHisProProGlnProSerLysArg 86
                                                                                                                                                                                                                                                                 53 yAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLeuTrpL 70
                                                                                                                                                                           44 GlyProValLeuHisLeu.....ProGlnMetGl 53
                                                                                     34 .....TrpThrLeuAsnSerAlaGlyTyrLeuLeu... 43
28 sArgGlyArgGlyGly......33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/1/ina/6B_COMB.seq:US-08-905-223-203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 203, Application US/08905223
Sequence 203, Application US/08905223
Sequence 203, Application US/08905223
Setent No. 6222029
GENERAL INFORMATION:
APPLICANT: Dealert, Aymeric
APPLICANT: Dealert, Aymeric
APPLICANT: Lacroix, Bruno
TITLE OF INVENTION: 5' ESTS FOR SECRETED PROTEINS
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 501 West Broadway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905, 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
TELEFAX: (619) 235-0176
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
LENGHH: 491 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: DOUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: ISTAELSEN, Ned A.
REGISTRATION NUMBER: 29,655
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Win95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abbara
STREET: Dor
CITY: San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 92101-3505
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Word
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9449 AA 9448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          120 ln 120
```

TOPOLOGY: LINEAR

```
89 ......GCCCCTGCACCTCATGGC......TCTG 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 oAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 laGlyTyrLeuLeuGlyProVal......LeuHiSLeuPro..... 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             211 TCTT ..... 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96 GlulleGlyGlyLysAlaArgLysHisArgArgGluThrProThrGlyGl 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              112 uGlyGluGlnGlySerGlyArgGlnSerLeuGluAspLeuGlyMetLeuS 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62 aLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProTyrSerH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           227 ......GGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGC 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           268 TGGGCTGCGGAACCGGAGCDACTTTCAGTTCTACCCACCGGG...CTGC 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                79 isProProGlnProSerLysArgAsnValMetGluThrPheAlaLysPro 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
Quality: 77.50 Length: 144
Ratio: 1.174 Gaps: 8
Percent Similarity: 45.833 Percent Identity: 31.944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-905-223-203 from: 1 to: 491
                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: sig_peptide
LOCATION: 39..107
IDENTIFICATION METHOD: Von Heijne matrix
OTHER INFORMATION: score 7.5
OTHER INFORMATION: seq LVLLLTEPLHLMA/LL
                                                                                                                                                                                                                                   NAME/KEY: other
LOCATION: 19..126
IDENTIFICATION METHOD: blastn
OTHER INFORMATION: identity 99
OTHER INFORMATION: region 57..164
OTHER INFORMATION: id 760981
OTHER INFORMATION: est
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 erMetLysIleProLysGluGluAspValLeu 139
:: ::|||::: ||||
                                                                                                                                             OTHER INFORMATION: identity 99
OTHER INFORMATION: region 170..289
OTHER INFORMATION: id T60981
OTHER INFORMATION: est
                                                                                       NAME/KEY: other
LOCATION: 132..251
IDENTIFICATION METHOD: blastn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-689-911-2 x US-08-905-223-203
                                Homo Sapiens
                                                  TISSUE TYPE: Brain
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: HOMO Sap
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-905-223-203
```

*

315 AGGTCACCTGCCTAGACCCAAATCCCCACTT 346

```
1 atggetectecetecgtece.....aagatgtectgaagteatag 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/geneseq/geneseqn/NA1980.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1981.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1982.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                  1861242
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                          930621 seqs, 428662619 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Listing first 45 summaries
                                                                               OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                   IDENTITY_NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                   US-09-689-911-1
                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                    Searched:
                                                                                                                                                                                                                                                  Sequence:
                                                                                                                            Run on:
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDSI/gcddata/geneseq/geneseqn/NA1998.DAT:*/SIDSI/gcddata/geneseq/geneseqn/NA199.DAT:*/SIDSI/gcddata/geneseq/geneseqn/NA2000.DAT:*/SIDSI/gcgdata/geneseq/geneseqn/NA2001.DAT:*/SIDSI/gcgdata/geneseq/geneseqn/NA2001.DAT:*

/SIDSI/gcgdata/geneseq/geneseqn/NA1992.DAT:*/SIDSI/gcgdata/geneseq/geneseqn/NA1993.DAT:*/SIDSI/gcgdata/geneseq/geneseqn/NA1994.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn/NA1995.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1996.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn/NA1997

/SIDSI/gcgdata/geneseq/geneseqn/NA1989. DAT:*/SIDSI/gcgdata/geneseq/geneseqn/NA1990.DAT:*

/SIDS1/gcgdata/geneseg/geneseqn/NA1988.DAT:*

/SIDS1/gcgdata/geneseq/geneseqn/NA1983.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1984.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1985.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1986.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1987.DAT:*/SIDS1/gcgdata/geneseq/geneseqn/NA1987.DAT:*/

/SIDS1/gcgdata/geneseq/geneseqn/NA1991.DAT:*

SUMMARIES

	Description	Galanin family pro	Galanin family pro	Receptor binding p	pGR2PL6 cDNA seque	Receptor binding p	Receptor binding p	DNA encoding a hum	pgR2PL3 cDNA seque	Plasmid pGR2PL6 DN	Receptor binding p	DNA encoding a rat
	ID	AAD04547	AAD04548	AAZ25536	AAZ25530	AAZ25535	AA225534	AAF44071	AAZ25531	AAZ25537	AAZ25533	AAF44070
	B.	22	22	50	20	20	20	22	20	20	20	22
	Query Match Length DB	426	351	473	974	695	180	180	1007	356	180	180
æ	Query Match 1	100.0	9.69	9.69	43.2	43.1	42.3	42.3	40.8	40.2	30.4	30.4
	Score	426	296.4	296.4	184.2	183.6	180	180	173.8	171.2	129.4	129.4
	Result No.		10	. ~	7	· LC	ı vc		- α	σ	10	11

10-OCT-2000; 2000WO-US27922.

O	2 '	encoaing	(human	(naman		Rat galanin recept	Nested PCR primer	Rat galanin recept	Nested PCR primer	Sequence encoding	DNA encoding human	Rat galanin cDNA n		Bovine endothelial	Human cDNA clone (Human cDNA sequenc	Human protein phos	Human cDNA encodin		Human ORFX ORF402	Human multiple tar				Human receptor-rel	Endothelial nitrog	_	Human T-type volta	Human protein enco	Human polynucleoti		G prote	HSV-2 strain SB5 C
AAZ25542	AA225532	AAF44069	AAF44065	AAF44067	AAF44068	AAZ25526	AAF44077	AAZ25527	AAF44078	AA028890	AAQ27236	AAZ88387	.AAT16858	AAT16857	AAH04852	AAH14623	AAF30484	AAF93820	AAF29348	AAC74847	AAF20842	AAA34720	AAX55272			AA094255		AAX83489	AAH99792	AAI612			AAV62147
20	50	22	22	22	22	20	22	20	22	3	13	21	17	17	22	22	22	22	22	21	2	21	20	70	21	16	22	20	22	22	20	22	19
126	180	180	267	567	267	86	86	800	86	575	740	672	3616	4089	751	2568	2924	2981	2981	6863	7800	7800	7803	114955	_	4097	2040	6132	1906	1906	1925	3517	28
· m	æ	æ	ထ	œ	σ) (T	, (*	\cdot	10		0.0	, 0	0.6	. 0		0 00	α	9 00	0 00	000	0 00	. 8	. 8	8.3	8.3	00	2 0	8 .	7.8	7.8	. 6	7.8	7.8
122.8	120.8	20.	119.2	19	6	יט וי		. L	11.0	1	4 4	39.6	200	4.86	3.6	3 0	9 (4	3 6	9 6	3.0	10	35.4	10	10	10		\		٠,	٠, ٠	٠ ٣	33.2	س
12	13	14	15	16	17	٠ ر ۲	9 0	20	2 5	1 0	2 6	24	2,5	10	200	, α , α	0 0	20	3 5	1 6	9 6	34	, L		3.5		0 0	0 4	-	10	7 7	77	45
													c	ه د	, (י כ	י נ)			ţ	ى ر	ינ	י כ) C) (ر	c	, (י נ	, ر	J	ပ

ALIGNMENTS

AAD04547 standard; cDNA; 426 BP

AAD04547

RESULT

of the

```
The present sequence is a cDNA encoding novel human protein (NHP) which shares sequence similarity with galanin proteins. Galanins are biologically active peptides that are present in the central and peripheral nervous system and are upregulated after spinal injury and in response to oestrogen. NHP is useful for diagnosis, drug screening, clinical trial monitoring and treatment of physiological disorders and imbalance. Galanins have been associated with for example regulating body weight, modulating behaviour, treating pain, inflammation, neuronal diagrams. Alzheimer's dementia, inflammatory bowel disease and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 actccagcatccgcacctgcccaccggggacgaggaggctggaccctcaatagtgctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acagcccttgagatcctagacctgtggaaggccatcgatgggctccctactcccaccct 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181 acagcccttgagatcctagacctgtggaaggccatcgatgggctcccctactcccaccct 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 atggctcctccctccgtccccctggtcctcctctcttgctgagcctggcaga 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atggetectecetecgtececetggtectectectegtectettgetgageetggeagag 60
                                                                                                                                          New nucleic acid sequence encoding a protein similar to proteins of galanin family, useful for screening for molecules with therapeutic,
                                                                               Sands AT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            agcttagaggatctgggcatgctcagcatgaaaattcccaaggaggaagatgtcctgaag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 426;
                                                                          Hilbun E, Zambrowicz B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 426 BP; 107 A; 127 C; 120 G; 72 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 426; DB 22; 100.0%; Pred. No. 2.3e-109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                        galanin family, useful for screening for mo
diagnostic and pharmacogenic applications -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                    Claim 1; Page 25; 29pp; English.
                                                                          Wang X,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAD04548 standard; cDNA; 351 BP.
                                          (LEXI-) LEXICON GENETICS INC.
                99US-0158848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 426; Conservative
                                                                         Donoho G,
                                                                                                  WPI; 2001-300218/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                  P-PSDB; AAE01017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  421 tcatag 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tcatag 426
                                                                      Turner CA,
                                                                                                                                                                                                                                                                                                                                                               disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAD04548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD04548
· DD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  рp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ά
```

ö

Gaps

```
ő
                                                                                                                                                          analgesic; anoretic; antianoretic; therapy; novel human protein; NHP; galanin; drug screening; physiological disorder; body weight regulation; behaviour modulation; pain; inflammation; neuronal repair; Alzheimer's dementia; inflammatory bowel disease; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is a cDNA encoding novel human protein (NHP) which shares sequence similarity with galanin proteins. Galanins are biologically active peptides that are present in the central and peripheral nervous system and are upregulated after spinal injury and in response to oestrogen. NHP is useful for diagnosis, drug screening in response trial monitoring and treatment of physiological disorders and imbalance. Galanins have been associated with for example regulating body weight, modulating behaviour, treating pain, inflammation, neuronal repair, Alzheimer's dementia, inflammatory bowel disease and infectious
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 actocagcatccgcacctgcccacogggacgaggaggctggacctcaatagtgctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 actccagcatccgcacctgcccaccggggacgaggagggtggaccctcaatagtgctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /*tag= a /product= "Novel human protein (NHP) #2 which share sequence similarity with galanin proteins"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid sequence encoding a protein similar to proteins of galanin family, useful for screening for molecules with therapeutic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                              Human; nootropic; neuroprotective; antimicrobial; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wang X, Hilbun E, Zambrowicz B, Sands AT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= "Mature novel human protein (NHP) #2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 69.6%; Score 296.4; DB 22; Length 351; Best Local Similarity 98.0%; Pred. No. 2.7e-73; Matches 300; Conservative 0; Mismatches 6; Indels 0;
                                                             Galanin family protein, novel human protein (NHP) cDNA #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 351 BP; 77 A; 115 C; 91 G; 68 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnostic and pharmacogenic applications -
                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 26; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (LEXI-) LEXICON GENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2000; 2000WO-US27922
17-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1..96
/*tag= b
97..348
/*tag= c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Turner CA, Donoho G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-300218/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAE01018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200127273-A1.
                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-APR-2001
   NAME OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        òγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P
```

g

g δ q δ

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV45154 and AAV255518 to AAV25552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                              181 acagccottgagatcotagacotgtggaaggccatcgatgggctcccctactccaccct 240
                               181 acagceettgagateetagaeetgtggaaggeeategatgggeteceetaeteeeaceet 240
                                                                                                                                                                                                                                                                                                                                                                                 Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69.6%; Score 296.4; DB 20; Length 473; 98.0%; Pred. No. 3e-73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ogi K, Kitada C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 473 BP; 96 A; 155 C; 124 G; 98 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                  Receptor binding peptide encoding cDNA SEQ ID NO:42.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 143; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                        AAZ25536 standard; cDNA; 473 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98JP-0078139.
98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP01482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                          21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kidney functioning -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-572170/48.
                                                                                                                                          301 gccagg 306
                                                                                                                                                                          301 ggcatg 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09948920-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohtaki T,
                                                                                                                                                                                                                                                                                           AAZ25536;
                                                                                                                                                                                                                                           AAZ25536
```

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin planding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV45154 and AAV25518 to AAV255252 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                    121 taccttctgggtcccgtcctccaccttccccaaatgggtgaccaagacggaaaggggag 180
                                                                                                                143 actccagcatccgcacctgcccaccggggacgaggaggaggctggaccctcaatagtgctggc 202
                                                                                                                                                                                                                                                                                                                                                                                                                                             Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                     203 taccttctgggtcccgtcctccaccttccccaaatgggtgaccaagacggaaagaggag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 974 BP; 258 A; 278 C; 229 G; 209 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ပဲ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohtaki I, Matsui H, Ishibashi Y, Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 13; Page 135; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                      AAZ25530 standard; cDNA; 974 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0078139.
98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             pgR2PL6 cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-572170/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P-PSDB; AAY45143
                                                                                                                                                                                                                                       301 gccagg 306
                                                                                                                                                                                                                                                                   383 ggcatg 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9948920-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                      AAZ25530;
                                                                                                                                                                                                                                                                                                             RESULT
AAZ25530
                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                          Qγ
                                                                                                                                                                                                                                                                   qq
                                                                                             qq
                                                                                                                           ŏλ
                                                                                                                                                     pp
                                                                                                                                                                                  δ
```

ó

0;

Indels

9;

0; Mismatches

Conservative

Best_Local Similarity Matches 300; Conserv

Dp ò

Query Match

```
;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which
                                                                 gacgaggaggctggaccctcaatagtgctggctacctctgggtcccgtcctccaccttc 148
                                                                                                                    149 cccaaaatgggtgaccaagacggaaagagggagacagcccttgagatcctagacctgtgga 208
                                                                                                                                                                         aggocatogatgggetecectacteceaecetecacagecetecaagaggaatgtgatgg 268
                                                                                                                                                                                                                                                               agacgtttgccaaaccagagattggaggtaaagccaggaaacacagaagagagacaccga 328
                                                                                                                                                                                                                                                                                     297 agactitogocaaaccagactciggagtaacaittgiiggagticcigacgiggigccgt 356
                                                                                                                                                                                                                                                                                                                                          357 ggaaacgaatccgaccaggaactacgagg-----tttcagatctaggcaagctctgca 409
                                     Gaps
                                                 29 tectectegtectettgetgageetggeagagaetecageateegeaeetgeeeaeggg 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                        329 caggagagagggaacaaggaagtggcaggcagagcttagaggatctgggcatgctcagca
                                  7;
43.2%; Score 184.2; DB 20; Length 974;
68.5%; Pred. No. 6.8e-42;
tive 0; Mismatches 118; Indels 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Receptor binding peptide encoding cDNA SEQ ID NO:41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kitada
                                                                                                                                                                                                                                                                                                                                                                    389 igaaaaticccaaggaagaagatgiccigaagicata 425
                                                                                                                                                                                                                                                                                                                                                                                            410 agaacgttccaaaggagaaagatgccttgccgtcata 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 13; Page 143; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ25535 standard; cDNA; 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-JP01482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98JP-0078139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LID.
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-572170/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1998;
21-SEP-1998;
                      Matches 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1999.
Query, Match
Best local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ohtaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ25535;
                                                                                                      83
                                                                                                                                                                                                            209
                                                                                                                                                                                                                                                               269
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                         g
                                                 ò
                                                                                                     ò
                                                                                                                            P
                                                                                                                                                       ŏ
                                                                                                                                                                                a
                                                                                                                                                                                                          òγ
                                                                                                                                                                                                                                q
                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                         pp
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
```

```
ó
bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV25158 to AAV2552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 egcacetgeccaceggggacgagggggctggacecteatagtgctggetacettetggg 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     254 tectgtectecacetttecteaaaggecaaceagggeaggaagaeagaeteagetettga 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tecegteetecacetteeceaaatgggtgaecaagaeggaaagagggagaecegeettga 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gatoctagacotgtggaaggocatogatgggotococtactocococotocagocoto 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               314 gatcctagacctgtggaaggccatagatgggctcccttattcccgctctccaaggatgac 373
                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12 ctocgtccccctggtcctcctcgtcctctggtgggcggagagctccagcatc 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  e.g. improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Physiologically active peptide; receptor binding; galanin receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GALR1, GALR2, GALR3, chymotrypsin, ligand, preprogalanin; galanin, drug development, memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                   Score 183.6; DB 20; Length 695;
Pred. No. 9e-42;
0; Mismatches 64; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           252 caagaggaatgtgatggagacgtttgccaaaccagagattggaggt 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Peptides binding to galanin receptor proteins, used to,
                                                                                                                                                                                                                                                Sequence 695 BP; 196 A; 201 C; 143 G; 155 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor binding peptide encoding cDNA SEQ ID NO:40.
                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 142; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ohtaki T, Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAZ25534 standard; cDNA; 180 BP
                                                                                                                                                                                                                                                                                                                                                      43.18;
77.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98JP-0078139
                                                                                                                                                                                               of the present invention,
                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 77.6 Matches 222; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-572170/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO9948920-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1999,
                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAZ25534;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAZ25534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
      8.833333388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACCOUNTY OF THE PLANT OF THE PL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   g
```

ö

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAX45154 and AAZ55518 to AAZ5552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the present invention.
```

8×8888888888×8

Sequence 180 BP; 37 A; 66 C; 47 G; 30 T; 0 other;

```
ö
                                                                                                                                                                                           133 cccgtcctccaccttccccaaatgggtgaccaagacggaaagagggagacagcccttgag 192
                                                                                                                                                             61 ccogtcctccaccttccccaaatgggtgaccaagacggaaagagggagacagccttgag 120
                                                          73 gcacctgcccaccggggacgaggaggctggacctcaatagtgctggctaccttctgggt 132
                                                                                          1 gcacctgcccaccggggacgaggaggctggaccctcaatagtgctggctaccttctgggt 60
                               0; Gaps
Length 180;
                                Indels
42.3%; Score 180; DB 20;
100.0%; Pred. No. 5.8e-41;
tive 0; Mismatches 0;
                                  Matches 180; Conservative
      Query Match
Best Local Similarity
                                                                                                                                                                      Ω
                                                                                                                                                                                                       δ
                                                                                                                                       ò
                                                                        δ
```

ω

RESULT

Physiologically active protein; galanin receptor; GALR; FGF; DNA encoding a human physiologically active protein. AAF44071 standard; DNA; 180 BP fibroblast growth factor; ds 23-MAR-2001 (first entry) Hono sapiens. AAF44071; AAF44071 RESULT

99JP-0080303. 99JP-0080303. JP2000270871-A. 24-MAR-1999; 24-MAR-1999; 03-OCT-2000

WPI; 2001-019315/03.

(TAKE) TAKEDA CHEM IND LTD.

Preparation of a new physiologically active peptide having a cleaved cysteine residue as N-terminal $\,$

Disclosure; Page 36; 44pp; Japanese.

This invention relates to a method for the preparation of a physiologically active peptide having a cleaved cysteine residue at the end N-terminal, and has any of the amino acid sequences given in AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153 including galanin receptors, and basic fibroblast growth factor. DNA sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are used in the isolation and characterisation of DNA encoding the proteins of the invention.

```
Sequence 180 BP; 37 A; 66 C; 47 G; 30 T; 0 other;
```

```
73 gcacctgcccaccggggacgaggaggctggacctcaatagtgctggctaccttctgggt 132
                                                                                                                                                                          61 cccgtcctccaccttccccaaatgggtgaccaagacggaaaggaggagacagccttgag 120
                                                                                                                                          133 cccgtcctccaccttccccaaatgggtgaccaagacggaaagagggagacagccttgag 192
                                  0; Gaps
                                                                                                      1 gcacctgcccaccgggggacgaggaggctggaccctcaatagtgctggctaccttctgggt 60
Length 180;
                                     Indels
42.3%; Score 180; DB 22;
100.0%; Pred. No. 5.8e-41;
tive 0; Mismatches 0;
         Query Match 42.3%
Best Local Similarity 100.0
Matches 180; Conservative
                                                                                                                                                                                                                                                           g
                                                                                                                                                                                         g
                                                                                                                                                                                                                           δŏ
```

Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss. AAZ25531 standard; cDNA; 1007 BP 21-DEC-1999 (first entry) pGR2PL3 cDNA sequence. AAZ25531; AAZ25531

WO9948920-A1 30-SEP-1999. Sus scrofa.

99WO-JP01482. 98JP-0078139 98JP-0266972 (TAKE) TAKEDA CHEM IND LTD 24-MAR-1999; 25-MAR-1998; 21-SEP-1998;

Ogi K, Ohtaki T, Matsui H, Ishibashi Y, WPI; 1999-572170/48

P-PSDB; AAY45144.

Peptides binding to galanin receptor proteins, used to, e.g. improve kidney functioning

Claim 13; Page 136; 153pp; Japanese.

The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, appetite improvers, and function requlators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV45154 and AAZ25518 to AAZ2552 represent sequences used in the exemplification of the present invention.

Sequence 1007 BP; 256 A; 293 C; 244 G; 214 T; 0 other;

Query Match

DB 20; Length 1007; 40.8%; Score 173.8;

```
5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which
                                                               97 tcgttcttgcagtcctgctcagcctgatggagtctccagcctctgctccggtccacaggg 156
                                                                                          89 gacgaggaggctggaccctcaatagtgctggctaccttctgggtcccgtcctccaccttc 148
                                                                                                           aggocattgatgggctcccctatccccagtctcagttggcctccaagaggagtctg-ggg 335
                                                                                                                                                                                                                                                         269 agacgittgccaaaccagagattggaggtaaagccaggaaacacagaagagagacaccga 328
                                                                                                                                                                                                                                                                                                             329 caggagagaggaacaaggaagtggcaggcagagcttagaggatctgggcatgctcagca 388
                                                                                                                                                                                                                                                                                                                                     396 ggaaacgaatccgaccaggaactacgagg-----tttcagatctaggcaagctctgca 448
                     Gaps
                                      29 tectectegtectettgetgageetggeagagaetecageateegeaeetgeeeaeggg 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                cocaaatgggtgaccaagacggaaagaggagacagcccttgagatcctagacctgtgga
                                                                                                                                                                                                    aggocatcgatgggctccctactcccacccccccacagccctccaagagaatgtgatgg
                                                                                                                                                                                                                                                                                   agactitogccaaaccagactctggagtaacatttgttggagttcctgacgtggtgccgt
                     8;
 Pred. No. 5.5e-39;
0; Mismatches 117; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ΰ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kitada
                                                                                                                                                                                                                                                                                                                                                                 389 tgaaaattcccaaggaggaagatgtcctgaagtcata 425
                                                         449 agaacgttccaaaggagaaagatgccttgtcgtcata 485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 18; Page 144-145; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP.
68.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid pGR2PL6 DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ25537 standard; DNA; 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-JP01482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98JP-0078139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98JP-0266972
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
               Conservative
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-572170/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO9948920-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohtaki T,
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ25537;
            Matches
                                                                                                                     157
                                                                                                                                                149
                                                                                                                                                                          217
                                                                                                                                                                                                      209
                                                                                                                                                                                                                                                                                   336
                                                                                                                                                                                                                                                                                                                                                                                                                                              AA225537
                                      δ
                                                             qq
                                                                                          à
                                                                                                                    a
                                                                                                                                               δ
                                                                                                                                                                       g
                                                                                                                                                                                                    δ
                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                        ò
                                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                              ð
                                                                                                                                                                                                                                                                                                                                    q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                              H
```

```
ö
bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin binding, such as memory function improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAV45129 to AAV45154 and AAZ25518 to AAZ2552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                     gacgaggaggctggaccctcaatagtgctggctacctctgggtcccgtcctccaccttc 148
                                                                                                                                                                                                                                                                                                    149 cccaaatgggtgaccaagacggaaagagggagacagccttgagatcctagacctgtgga 208
                                                                                                                                                                                                                                                                                                                                                                                                       209 aggocatcgatgggctccctactcccacctccacagcctccaagaggaatgtgatgg 268
                                                                                                                                                                                                                                                                                                                                                                                                                                   203 aggccattgatgggctcccctatccccagtctcagttggcctccaagaggagtctggggg 262
                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                   88
                                                                                                                                                                                                                                                      23 tegitetigeagicetgeteageetgaigagietecageetetgeteeggieeaaggg 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                                                                                                                                                                                                                           29 tectectegtectettgetgageetggeagagetecageateegeacetgeecaeeggg
                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                 40.2%; Score 171.2; DB 20; Length 356; 76.8%; Pred. No. 2.1e-38; Live 0; Mismatches 63; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΰ
                                                                                                                      Sequence 356 BP; 67 A; 104 C; 108 G; 77 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor binding peptide encoding cDNA SEQ ID NO:39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogi K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agacgtttgccaaaccagagattggaggtaaa 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263 agactttcgccaaaccagactctggagtaaca 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 11; Page 142; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAZ25533 standard; cDNA; 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98JP-0078139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TAKE ) TAKEDA CHEM IND LTD.
                                                                                         of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                              Conservative
                                                                                                                                                                             Local Similarity
nes 209; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1999-572170/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO9948920-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus sp.
                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohtaki T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAZ25533;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10
                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
 8×8888888
                                                                                                                                                                                                                           à
                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                         g
                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                   g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            g
```

```
The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially lidentical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin/galanin receptor binding function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAX45154 and AAX25518 to AAX2552 represent sequences used in the exemplification
                                                                                                                                                                                                                                                                                   of the present invention.
```

Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;

```
;
0
                          Gaps
                         0;
Score 129.4; DB 20; Length 180; Pred. No. 7.3e-27;
                          Indels
                          26;
                          0; Mismatches
  Query Match 30.4%;
Best Local Similarity 84.8%;
                           Conservative
                             Matches 145;
```

ecegiceiceaecticeceaaatgggitgaecaagaeggaaaagaggaagaecageectigag 192 cetgiceiceaectitecteaaaggecaaecaggeaggaagaagacagaeteageteitgag 120 geacctgeceaceggggaegaggaggetggaeceteaatagtgetggetaeettetgggt 132 133 61 qq οχ a

δ

AAF44070 standard; DNA; 180 BP 23-MAR-2001 (first entry) AAF44070;

Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds. DNA encoding a rat physiologically active protein.

Rattus sp.

JP2000270871-A.

99JP-0080303 24-MAR-1999; (TAKE) TAKEDA CHEM IND LTD

99JP-0080303

24-MAR-1999;

WPI; 2001-019315/03.

Preparation of a new physiologically active peptide having a cleaved cysteine residue as N-terminal $\,$ Disclosure; Page 35-36; 44pp; Japanese.

This invention relates to a method for the preparation of a physiologically active peptide having a cleaved cysteine residue at the end N-terminal, and has any of the amino acid sequences given in AAB651316. The invention includes sequences AAB65137 - AAB65137 which represent proteins related to the main proteins of the invention, including agalanin receptors, and basic fibroblast growth factor. DNA sequences AAR44055 - AAR44071 and PCR primers AAR44072 - AAR44086 are used in the isolation and characterisation of DNA encoding the proteins of the invention.

```
Sequence 180 BP; 39 A; 57 C; 47 G; 37 T; 0 other;
         S
```

```
133 occytectecacettececaaatgggtgaceaagaeggaaagagggagagaeettgag 192
                                                                         1 geacetgeteacaggggacgaggaggetggacceteaatagtgetggttacetectgggt 60
                          Gaps
                        ö
 22; Length 180;
                                                                                                                                                             26; Indels
                                                                                                                                                   193 atcctagacctgtggaaggccatcgatgggctcccctactcccacctcca
Score 129.4; DB 2
Pred. No. 7.3e-27;
0; Mismatches 26
  30.4%;
illarity 84.8%;
Conservative
               Best Local Similarity
Matches 145; Conserv
      Query Match
                                                                                                       ò
                                                                                                                              d
                                                                                                                                                       ò
                                                                                                                                                                             g
                                                        δ
```

ö

Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR2; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss. AAZ25542 standard; DNA; 126 BP 21-DEC-1999 (first entry) Human ligand PCR product. AAZ25542; RESULT 12 AAZ25542

99WO-JP01482. 98JP-0078139. 98JP-0266972. Homo sapiens. WO9948920-A1 25-MAR-1998; 21-SEP-1998; 24-MAR-1999; 30-SEP-1999. Synthetic

Ogi K, Ohtaki T, Matsui H, Ishibashi Y, (TAKE) TAKEDA CHEM IND LTD

Kitada C;

WPI; 1999-572170/48

e.g. improve Peptides binding to galanin receptor proteins, used to, kidney functioning

Example 19; Page 90-91; 153pp; Japanese.

The present invention describes peptides (I) binding to galanin receptor proteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of Grugs acting on galanin/galanin receptor binding function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAY45129 to AAX45154 and AAZ25518 to AAX2552 represent sequences used in the exemplification of the present invention.

Sequence 126 BP; 30 A; 35 C; 36 G; 25 T; 0 other;

g

Db δ

ŏ

1 gctccggtccacagggggggggggggggggggtggctcaacagtgctggttacctcctgggt 60

Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds.

JP2000270871-A.

DNA encoding a pig physiologically active protein.

(first entry)

23-MAR-2001

AAF44069:

AAF44069 standard; DNA; 180 BP

AAF44069

193 atcctagacctgtggaaggccatcgatgggctcccctactcccacctccacagccctcc

```
The present invention describes peptides (I) binding to galanin receptor jecteins. (I) contain the sequence APAHRGRGG or one substantially identical to it, and their precursors, salts, amides and esters, which bind especially to rat galanin receptor proteins. Products from the present invention are used in assays of galanin/galanin receptor binding and the development of drugs acting on galanin pinding, such as memory function improvers, appetite improvers, and function regulators for the womb, kidney, prostate, testis or skeletal muscle. AAV15129 to AAV45134 and AAZ25518 to AAX2552 represent sequences used in the exemplification
                                        96 aggetggaccetcaatagtgetggetacettetgggteeegteeteeacetteeeaat 155
                                                                                              Gaps
                                                       tides binding to galanin receptor proteins, used to, e.g. improve
                                                                                                                                                                                                                                                                                                                                                                     Physiologically active peptide; receptor binding; galanin receptor; GALR1; GALR3; chymotrypsin; ligand; preprogalanin; galanin; drug development; memory function; appetite improver; womb; kidney; function regulator; prostate; testis; skeletal muscle; ss.
                   .;
0
                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kitada C;
                5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 180 BP; 30 A; 59 C; 59 G; 32 T; 0 other;
 98.4%; Pred. No. 4.5e-25;
                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ogi K,
                                                                                                                                                                                                                                                                                                                                            Porcine ligand (1-60) encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 138; 153pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matsui H, Ishibashi Y,
                                                                                                                                                                                                                                                    AAZ25532 standard; cDNA; 180 BP.
               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98JP-0266972.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-JP01482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98JP-0078139
                                                                                                                                                                                                                                                                                                                (first entry)
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1999-572170/48.
 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ney functioning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P-PSDB; AAY45145
                                                                                                                                                       216 cgatgg 221
                                                                                                                                                                                 121 agatgg 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9948920-A1.
                                                                                                                                                                                                                                                                                                                21-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ohtaki T,
                                                                                                                                                                                                                                                                                    AAZ25532;
Local
                                                                                                                                                                                                                              RESULT 13
                                                                                                                                                                                                                                                                                  q
                                                                                                ò
                                                                                                                                                                               q
```

```
73 gcacctgcccaccggggacgaggaggctggacctcaatagtgctgctaccttctgggt 132
                                                                                                                        133 cccgtcctccaccttccccaaatgggtgaccaagacggaaagaggagacagccttgag 192
                                                                                                                                                     61 cccgtactccatccgccctccagggctgaaggaggcgggaaggggaagacagcctcggg 120
                                                                                                                                                                                                    193 atcctagacctgtggaaggccatcgatgggctcccctactcccacctccacagccctcc
                                   ö
   DB 22; Length 180;
Score 120.8; DB 22; Length
Pred. No. 1.8e-24;
0; Mismatches 37; Indels
 28.48;
79.48;
                                Conservative
              Local Similarity
                              143;
Query Match
                                Matches
                                                                                         g
                                                                                                                        Qγ
                                                                                                                                                     g
                                                                                                                                                                                  οy
```

QQ

ö

Gaps

;

37; Indels

Mismatches

ö

Best Local Similarity '2...
Matches 143; Conservative

ô

Query Match

DB 20; Length 180;

28.4%; Score 120.8; DB 2 79.4%; Pred. No. 1.8e-24;

73 gcacctgcccaccggggacgaggaggctggaccctcaatagtgctggctaccttctgggt 132

This invention relates to a method for the preparation of a physiologically active peptide having a cleaved cysteine residue at the end N-terminal, and has any of the amino acid sequences given in AAB65131 - AAB65135. The invention includes sequences AAB65137 - AAB65153 which represent proteins related to the main proteins of the invention, including galanin receptors, and basic fibroblast growth factor. DNA sequences AAR44065 - AAR44071 and PCR primers AAR44072 - AAR44086 are used in the isolation and characterisation of DNA encoding the proteins

Sequence 180 BP; 30 A; 59 C; 59 G; 32 T; 0 other;

of the invention.

Preparation of a new physiologically active peptide having a cleaved

99JP-0080303.

24-MAR-1999; 24-MAR-1999;

03-OCT-2000.

(TAKE) TAKEDA CHEM IND LTD

WPI; 2001-019315/03.

Disclosure; Page 35; 44pp; Japanese.

cysteine residue as N-terminal

ó

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for the preparation of a physiologically active peptide having a cleaved cysteine residue at the and N-terminal, and has any of the amino acid sequences given in AAB65131 - AAB65136. The invention includes sequences AAB65137 - AAB65153 which represent proteins related to the main proteins of the invention, including galanin receptors, and basic fibroblast growth factor. DNA sequences AAF44065 - AAF44071 and PCR primers AAF44072 - AAF44086 are used in the isolation and characterisation of DNA encoding the proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 occgiociocaccitococaaaigggigaccaagacggaaagagggagacagcciigag 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              448 cccgtactccatccgccctccagggctgaaggaggcgggaaggggaagacagccctcggc 507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Preparation of a new physiologically active peptide having a cleaved cysteine residue as N-terminal \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; Length 567;
                                                                                                               bFGF (human fibroblast growth factor) DNA sequence SEQ ID 15.
                                                                                                                                            Physiologically active protein; galanin receptor; GALR; FGF; fibroblast growth factor; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match
28.0%; Score 119.2; DB 22; Length
Best Local Similarity 78.9%; Pred. No. 7.3e-24;
Matches 142; Conservative 0; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 567 BP; 134 A; 153 C; 163 G; 117 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 7; 44pp; Japanese.
                           AAF44065 standard; DNA; 567 BP.
                                                                                                                                                                                                                                                                                    99JP-0080303.
                                                                                                                                                                                                                                                                                                                   99JP-0080303.
                                                                                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEM IND LTD.
                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-019315/03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
                                                                                                                                                                                                                             JP2000270871-A.
                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                                                                                                                                                                   24-MAR-1999;
                                                                                                                                                                                                                                                                                      24-MAR-1999;
                                                                                       23-MAR-2001
                                                                                                                                                                                                                                                           03-OCT-2000.
                                                          AAF44065;
15
               AAF44065
 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        g
                               δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ò
```

Search completed: March 2, 2002, 23:56:26 Job time: 5947 sec

	-			
•				
7				
•				

```
March 2, 2002, 20:57:26; Search time 75 Seconds (without alignments) 1286.395 Million cell updates/sec
                                                                                                                                                                                                                                                                                 1 atggctcctccctccgtccc.....aagatgtcctgaagtcatag 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                       702406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                          351203 seqs, 113238999 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Listing first 45 summaries
                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                         IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Issued_Patents_NA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Post-processing: Minimum Match 0% Maximum Match 100%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                            US-09-689-911-1•
                                                                                                                                                                                                                                                                                                                                           Scoring table:
                                                                                                                                                                                                                                                                          Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Database :
                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                   Sednence:
                                                                                                                                                                                                                                                   Title:
```

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	200 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	sednence 13, Appr
SUMMARIES	08 - 507 - 016 - 007 - 016 - 007 - 008 - 2463 - 007 - 008 - 2463 - 007 - 008 - 2463 - 008 - 2463 - 008 - 2463 - 008 - 2463 - 008 - 2463 - 008 - 2463 - 008 - 2673	US-08-773-251-13
DB		7
% Query Match Length I	444 444 447 447 447 447 447 447 447 447	1045
% Query Match	000 000 000 000 000 000 000 000	6.9
Score	46 46 46 46 46 46 46 46 46 46 46 46 46 4	29.4
<u>.</u> بـ	11 22 33 33 33 34 44 44 11 11 11 11 11 11 11 11 11 11 11	27
Result No.	000000 0 00 00 0	

Sequence 14, Appl Sequence 12, Appl Sequence 7, Appli Sequence 1, Appli Sequence 14, Appli Sequence 14, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 77, Appli Sequence 89, Appli	12221
US-08-773-251-14 US-08-773-251-18 US-08-773-251-8 US-08-773-251-7 US-08-773-251-1 US-08-232-463-14 US-08-132-652-1 US-09-132-652-1 US-09-244-796-17 US-09-244-796-17	US-09-240-274-90 US-09-240-274-91 US-09-042-33-224 US-08-758-417A-72 US-08-053-131-120 US-08-645-641-120
000000mmma44	4444414
1086 2253 2803 2807 2959 7218 8802 8802 289 289	375 375 375 3618 3618 3699 3699
	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
44444444460000000000000000000000000000	2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.2.
222 332 332 334 337 337 337	4 4 4 4 4 5 5 6 5 6 6 6 6 6 6 6 6 6 6 6
000	υυυ

ALIGNMENTS

```
patent No. 5756460
| GENERAL INFORMATION:
| APPLICANT: EVANS, HELEN F. |
| APPLICANT: SHINE, JOHN |
| TITLE OF INVENTION: HUMAN GALANIN, CDNA CLONES ENCODING |
| TITLE OF INVENTION: HUMAN GALANIN AND A METHOD OF PRODUCING HUMAN GALANIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/507,016 FILING DATE: 25-JULY-1995 CLASSIFICATION: 435
                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
STREET: 555 THIRTEENTH STREET, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/108,733
FILING DATE: 03.5EP-1993
APPLICATION NUMBER: PCT/AU92/00097
FILING DATE: 06-MAR.1992
APPLICATION NUMBER: AU PK4953
FILING DATE: 06-MAR.1991
ATTORNEY/AGENT INFORMATION:
NAME: ERNST, BARBARA G:
REGISTRATION NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 30,377
REFERENCE/DOCKET NUMBER: 1871-117A
TELECOMMUNICATION INFORMATION:
TELEDOMONICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (202)783-6031
INFORMATION FOR SEQ ID NO: 8: SEQUENCE CHARACTERISTICS: LENGTH: 575 base pairs TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                         STREET: 555 THING CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                            D. C.
: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                    20004
                                                                                                                                                                                                                                                                                                                             COUNTRY:
US-08-507-016-8
                                                                                                                                                                                                                                                                                                            STATE:
```

```
Matches
                                                                                                                                                                                                                                                                                                                      ΟŊ
                                                                                                               ;
0
                                                                                                                                                                                                     61 actccagcatccgcacctgcccaccggggacgaggggggctggaccctcaatagtgctggc 120
                                                                                                                                                                                                                        1 atggetectecetecgtecectggtectectectegtecttgetgageetggeagag 60
                                                                                                                                                      ;
0
                                                                  10.8%; Score 46; DB 1; Length 575; Similarity 59.0%; Pred. No. 0.00011; 9; Conservative 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: Foley & Lardner
F: 1800 Diagonal Road, Suite 500
Alexandria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP 91 114 300.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                    US-08-232-463-14/c
Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 3047
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELERAN. 899119,
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
                                                   Query Match
Best Local Similarity 59.08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (703)836-9300
(703)683-4109
                                                                                                                                                                                                                                                                     121 taccttctgggtcc 134
                                                                                                                                                                                                                                                                                                  134 TACCTGCTGGGCCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
LOCATION: 14..385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : IMMEDIATE SOURCE: CLONE: PTZGPt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
ZIP: 22313-0299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ٧A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
   ;
US-08-507-016-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                  ò
```

DB 1; Length 7218;

10.7%; Score 45.4; DB 1.5%; Pred. No. 0.00051;

Best Local Similarity

Query Match

```
152 aaatgggtgaccaagacggaaagagggagacagccttgagatcctagacctgtggaagg 211
                                                                                                        212 ccatcgatgggctcccctactcccacctccacagcctccaagaggaatgtgatggaga 271
                                                                                                                                                                                272 cgtttgccaaaccagagattggaggtaaagccaggaaacacagaagagagacaccgacag 331
                                                                                                                                                                                                                                                         332 gagagggggaacaaggaagtggcaggcagacttagaggatctgggcatgctcagcatga 391
       Gaps
     ö
   98; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Harrison, David G.
APPLICANT: Alexander, R. Wayne
APPLICANT: Murphy, T.J.
APPLICANT: Nishida, Ken'ichi
TITLE OF INVENTION: Endothelial Nitric Oxide Synthase
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION DATA:
FILING DATE:
4; Conservative 167; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Kilpatrick & Cody
STREET: 1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                         1087 RRRRRRRRRRRRRRRRRRRRRATGGCAAG 1059
                                                                                                                                                                                                                                                                                                                                392 aaattcccaaggaggaagatgtcctgaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/07908245 Patent No. 5498539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION UNDBER: 31,284
REFERENCE/DOCKET UNBBER: EMU I TELECOMMUNICATION INFORMATION:
TELEFAX: 404-815-6508
TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4089 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; CELL TYPE: Endothelial US-07-908-245-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1992070
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: U.S.
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                          US-07-908-245-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
```

οy

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA EXPRESSION VECTORS FOR USE IN THE GENE THERAPEUTIC TREATMENT OF VASCULAR DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INCORNATION:
GENERAL INCORNATION:
APPLICANT: SCHRADER, Juergen
APPLICANT: SCHRADER, Axel
TITLE OF INVENTION: DNA EXPRESSION VECTORS FOR USE IN GENE THERAPEUTIC
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
CURRENT APPLICATION NUMBER: US/09/123,708
CURRENT APPLICATION NUMBER: 08/553,503
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
EARLIER FILING DATE: 1996-03-01
SCHEMER FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PALENTIN VET. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3217 GGGAGCAGCGGCAACACCAGGGTCATGGGGTGCGGCTGCAGCCCTTTGCTCTCAA 3158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 tecageateegeacetgeecaaceggggaegaggaggetggaeceteaatagtgetggeta 122
                                                                                                                                                                                                                                               3189 GGGAGCAGCGGCAACACCAAGGGTCATGGGGGCGGGCTGCAGCCCTTTGCTCTAA 3130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 ggetectectecgtececetggtectectectegtectetgetgagectggeagagae 62
                                                                                                                             3249 GGCCAAACACCCGGGCTCCTGGAGCTCCTCGCGGTAGAGATGGTCGAGTT 3190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Gaps
                                                                                                                                                                                                  63 tecageatecgeacetgeceaceggggaegaggaggaggetggaeeceteaatagtgetga 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3157 IGTCATGCAGCCTCTCCTGCCAAAATCCCCGGAAGGGGGCGATGCCAGTGCCAGGG 3102
                                                       Gaps
                                                                                                  3 ggctectecetecgteceetggteetectectegtectettgetgagectggeagagae 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3129 TGTCATGCAGCCTCTCCTGCCAAAATCCCCGGAAGGGGGCGATGCCAGTGCCAGGG 3074
                                                                                                                                                                                                                                                                                                     123 ccttctgggtcccgtcctccaccttccccaaatgggtgaccaagacggaaagagg 178
                                                     .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ouery Match
Best tocal Similarity 50.0%; Pred. No. 0.44;
Matches 88; Conservative 0; Mismatches 88; Indels 0
Query Match

9.0%; Score 38.4; DB 1; Length 4089;
Best Local Similarity 51.1%; Pred. No. 0.049;
Matches 90; Conservative 0; Mismatches 86; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRENT PAPLICATION NUMBER: US/09/123,624 CURRENT FILING DATE: 1998-07-28 PRIOR APPLICATION NUMBER: 08/553,503 PRIOR FILING DATE: 1996-03-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 5, Application US/09123624 Patent No. 6149936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/09123708 Patent No. 6146887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SCHRADER, JUTGEN
APPLICANT: SCHRADER, AXEL
TITLE OF INVENTION: TREATMEN
TITLE OF INVENTION: TREATMEN
FILE REPERENCE: 511169-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; ORGANISM: Cytomegalovirus
US-09-123-708-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-123-624-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-123-708-5/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    à
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                     3217 GGGAGCAGCGGCAACACCAGGGTCATGGGGTGCGGCTGCAGCCCTTTGCTCTCAA 3158
                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                 63 tecageatecgeacetgeceaceggggaegaggaggetggaeeceteaatagtgetggeta 122
                                                                                                                                                                                                                                                                                     3 gotteeteesteegteeceetggteeteetegteettgetgaggetggagagae 62
                                                                                                                                                                                                                                                   0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3157 TGTCATGCAGCCTCTCCTGCCAAAATCCCCGGAAGGGGGCGATGCCAGTGCCAGGG 3102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: KOrenberg, Julie R.
TITLE OF INVENTION: DUCLEIC ACID ENCODING CONGENITAL HEART
TITLE OF INVENTION: DISEASE PROTEIN AND PRODUCTS RELATED THERETO
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                               123 cettetgggteeegteetecaeetteeeaatgggtgaeeaagaeggaaagaggg 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                     Query Match

8.3%; Score 35.2; DB 3; Length 4097;
Best Local Similarity 50.0%; Pred. No. 0.44;
Matches 88; Conservative 0; Mismatches 88; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 32; DB 2; Length 216; 62.5%; Pred. No. 1.1; tive 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/927,307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION NUMBER: 4411402.8
PRIOR FILLING DATE: 1994-03-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/08927307
Patent No. 5945305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY, AGENT INFORMATION:
NAME: Ramos, Robert T.
REGISTRATION NUMBER: 37,915
REFERENCE/DOCKET NUMBER: P-C
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (619)535-9001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 62.59
Matches 50; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (619)535-8949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 216 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  California
: United States
                                     NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                         TYPE: DNA
CRGANISM: Bos taurus
US-09-123-624-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 San Diego
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 92122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-08-927-307-3/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-927-307-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                       LENGIH: 4097
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
```

ö

```
ö
0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 3, Application US/09385947
Patent No. 6040429
GENERAL INFORMATION:
APPLICANT: Rorenberg, Julie R.
TITLE OF INVENTION:
DISEASE PROTEIN AND PRODUCTS RELATED THERETO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match

Ouery Match

Best Local Similarity 62.5%; Pred. No. 1.1;

Matches 50; Conservative 0; Mismatches 30; Indels
                                                                                                                                                                                                                                                                                                              E: Campbell & Flores LLP
4370 La Jolla Village Drive, Suite 700
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IN P. Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/927,307
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Ramos, Robert T.
REGISTRATION NUMBER: 37,915
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: P-C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619)535-9001
TELEFAX: (619)535-8949
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                             63 tecageatecgeacetgeec 82
                                                                                             79 GGGGCCTTCACCACCTCTCC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                   Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63 tecageatecgeacetgeee 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79 GGGGCCTTCACCACCTCTCC 60
                                                                                                                                                                                                                                                                                                                                                                                United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 216 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                           CITY: San Diego
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                            US-09-385-947-3/c
                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-09-385-947-3
                                                                                                                                              RESULT
                             q
                                                               δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ô
```

```
ö
                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence
OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 280071 ggccggtcgagacgctttccgccgcaccggatcaccgcgccgccgcggcagcatcctcg 280130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Db 279958 ggccggtcgagacgctttccgccgcagcatcaccgcgccgccgcggcagcatcctcg 280017
              APPLICANT: WHITE, Owen R.
APPLICANT: FRAER, Claire M.
APPLICANT: FRAER, Claire M.
APPLICANT: VERNER, John C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM FITLE OF INVENTION: TUBERCULOSIS
FILE REPERBURE: 24366-22007, 00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER OF SEQ ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 gcctggcagagactccagcatccgcaccggggacgagggggggctggaccctca 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Own R.
APPLICANT: WHITE, Own R.
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
NUMBER FILES OF STEIN INS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 gectggcagagactccagcatccgcaccggggacgaggaggctggacctca 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
7.3%: Score 31.2; DB 4; Length 4403765;
Best Local Similarity 58.7%; Pred. No. 46;
Matches 54; Conservative 0; Mismatches 38; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 4411529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db 280131 acttgcttggcaacctcgttgcggccctgctc 280162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Db 280018 acttgcttggcaacctcgttgcggccctgctc 280049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7.3%; Score 31.2; DE 58.7%; Pred. No. 46; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           110 atagtgctggctaccttctgggtcccgtcctc 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 atagtgctggctaccttctgggtcccgtcctc 141
                                                                                                                                                                                                                                                                                                              ORGANISM: Mycobacterium tuberculosis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 1, Application US/09103840A; Patent No. 6294328
APPLICANT: FLEISCHMAN, Robert D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 58.79
Matches 54; Conservative
                                                                                                                                                                                                                                                                   LENGTH: 4403765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 4411529
                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-103-840A-1
                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
```

10

RESULT

```
δŽ
    DUSCH, Nicole
APPLICANT: Kalinowski, Jorn
APPLICANT: Publer. Alfred
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID USING STRAINS OF THE FAMILY ENTEROBACTERIACEAE
FILE REFRENCE: 21123/260203
CURRENT APPLICATION NUMBER: US/09/318,739A
CURRENT FILING DATE: 1999-05-26
PRIOR APPLICATION NUMBER: DE 1985314.5
PRIOR FILING DATE: 1998-12-01
NUMBER OF SEQ ID NOS: 6
SOFTMARE: PALENTITE
SEQ IN NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Dusch, Nicole
APPLICANT: Kalinowski, Jorn
APPLICANT: Publex: Alfred
TITLE OF INVENTION: METHOD FOR THE FERMENTATIVE PRODUCTION OF D-PANTOTHENIC
TITLE OF INVENTION: ACID BY ENHANCEMENT OF THE PAND GENE IN MICROORGANISMS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 agacggaaagaggagacagcccttgagatcctagacctgtggaaggccatcgatgggct 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             105 cctcaatagtgctggctaccttctgggtcccgtcctccaccttccccaaatgggtgacca 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 52.8%; Pred. No. 3.3;
Matches 67; Conservative 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 21123/260204
CURRENT APPLICATION NUMBER: US/09/318,793A
CURRENT FILING DATE: 1999-05-26
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09318793A Patent No. 6184007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; NAME/KEY: CDS
; LOCATION: (77)...(484)
US-09-318-793A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; LOCATION: (77)..(484)
US-09-318-739A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          427 eggeaac 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 cccctac 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-318-793A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      540
US-09-318-739A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      οy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pp
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Gaps
                                 165 agacggaaagaggagacagccttgagatcctagacctgtggaaggccatcgatgggct 224
 0; Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
7.2%; Score 30.8; DB 3; Length 2272;
Best Local Similarity 49.1%; Pred. No. 7;
Matches 109; Conservative 0; Mismatches 112; Indels 1;
 0; Mismatches 60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Bell, Graeme I
APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Razuki
TITLE OF INVENTION: Opioid Receptor Genes,
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/147,592A FILING DATE: 05-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Arnold, White & Durkee STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/08147592A
; Patent No. 6096513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37,259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 2272 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: N/A INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
         67; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12..1127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                427 cggcaac 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                               225 cccctac 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Texas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72210
                                                                                                                                                                                                                                                                                                      US-08-147-592A-3/C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION:
US-08-147-592A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
               Matches
```

ä

Score 31; DB 4; Length 540; Pred. No. 3.3;

7.3%; 52.8%;

Query Match Best Local Similarity

```
2195 GGAATCGAACCTATGCTCTCTGCAAGAGTCACGTGCCCTTAATCACTCAGCCACCTTT 2136
                                                                                                            2075 CTTGCTTTTGGGGCCCTTGTTCAGGATCCAGGGAGCCTCTGCTTCTGCCCACTGTCCACA 2016
67 gcatccgcacctgcccaccggggacgaggaggctggacctcaatagtgctggctacctt 126
                                                                                 127 ctgggtcccgtcctccaccttccccaaatgggtgaccaagacggaaagggggagacagcc 186
                                                                                                                                                                 187 cttgagatcctagacctgtggaaggccatcgatgggctcccctact-cccacctccaca 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 accgacaggagagagggaacaaggaagtggcaggcagagcttagaggatctgggcatgct 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: SZOSTGK, Jack W.
APPLICANT: SZOSTGK, Jack W.
APPLICANT: ROBDETCS, RICHARD W.
APPLICANT: MOBER: RICHARD W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: PUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT APPLICATION NUMBER: 06/035,963
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASLEGE for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Pest Local Similarity 30.9%; Pred. No. 3.7;
Matches 47; Conservative 47; Mismatches 56; Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3, Application US/09244796
Patent No. 6281344
GENERAL INFORMATION:
APPLICANT: Szostak, Jack W.
APPLICANT: Roberts, Richard W.
APPLICANT: Liu, Rihe
TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN
TITLE OF INVENTION: FUSIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          56; Indels
                                                                                                                                                                                                                                                                                        2015 GCCCACAGGGATACAGGCTGCGGGTTCTTCTAAACCAGA 1974
                                                                                                                                                                                                                                                  246 gccctccaagaggaatgtgatggagacgtttgccaaaccaga 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            384 cagcatgaaaattcccaaggaggaagatgtcc 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246 cruaaaaaaaaaaaaaaaaaaaaaaaacc 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Translation template US-09-007-005-3
                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 3, Application US/09007005B
; Patent No. 6258558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                            US-09-007-005-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 3
LENGTH: 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-09-244-796-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: RNA
                                                                                                                     a
                                                                                                                                                                                                      qq
                                                                                                                                                                 ò
                                                                                                                                                                                                                                                ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          δy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
```

```
264 gatggagacgtttgccaaaccagagattggaggtaaagccaggaaacacagaagagac 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 accgacaggagaggggaacaaggaagtggcaggcagagcttagaggatctgggcatgct 383
                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                          2;
                                                                                                                                                                                                                                                                                                                                                                                             7.1%; Score 30.4; DB 4; Length 277; 30.9%; Pred. No. 3.7; tive 47; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Stiles, Gary L.
APPLICANT: Ren, Hongzu
APPLICANT: Ren, Hongzu
APPLICANT: Olah, Mark E.
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kenneth D. Sibley; Bell, Seltzer, Park and
ADDRESSEE: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PatentIn Release #1.0, Version #1.25
            CURRENT APPLICATION NUMBER: US/09/244,796
CURRENT FILING DATE: 1999-02-05
BARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1997-11-06
EARLIER FILING DATE: 1998-01-14
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTERO FOR Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             384 cagcatgaaaattcccaaggaaggaagatgtcc 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   246 cruadadadadadadadadadadadadacc 277
                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Translation template US-09-244-796-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US/07/918,314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S-07-918-314-3/c
Sequence 3, Application US/07918314
Patent No. 5320962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Charlotte
No. 5320962th Carolina
RY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Sibley, Kenneth D.
REGISTRATION NUMBER: 31,665
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
FILE REFERENCE: 00786/350007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 575102
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 30.98
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 19920722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: U
ZIP: 28234
                                                                                                                                                                                                                SEQ ID NO 3
LENGTH: 277
                                                                                                                                                                                                                                                         TYPE: RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             à
```

	·	
		:

```
March 2, 2002, 20:57:21; Search time 1465.35 Seconds (without alignments) 4795.986 Million cell updates/sec
                                                                                                                     1 atggetectecetecgtece.....aagatgteetgaagteatag 426
                                                                                                                                                                                             2944280
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                          1472140 seqs, 8248589755 residues
                                                                                                                                                                                                                                                 Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                         OM nucleic - nucleic search, using sw model
                                                                                                                                              IDENTITY_NUC Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               em_un:*
em_vi:*
em_htgo_hum:*
em_htgo_inv:*
em_htgo_rod:*
em_htg_hum:*
em_htg_hum:*
em_htg_huw:*
em_htg_how:*
                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                       gb_pl:*
gb_pr:*
gb_pr:*
gb_ro:*
gb_sts:*
gb_un:*
gb_vi:*
em_ba:*
em_fun:*
                                                                                                      US-09-689-911-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  em_ro:*
em_sts:*
em_sy:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     em_pat:*
em_ph:*
em_pl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              em_in:*
em_om:*
em_or:*
                                                                                                                                                                                                                                                                                                              gb_htg:*
gb_in:*
                                                                                                                                                                                                                                                                                                                                gb_om:*
gb_ov:*
gb_pat:*
gb_ph:*
                                                                                                                                                                                                                                                                                                    gb_ba:*
                                                                                                                                                                                                                                                                                         GenEmbl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                      Perfect score:
                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                            Database :
                                                                                                                               Sednence:
                                                                                                                                                                             Searched:
                                                                  Run on:
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AX112343 Sequence AX11245 Sequence AX11245 Sequence AX188492 Homo sapi AF188499 Sus scrof AF188491 Rattus no AC023887 Homo sapi AC011506 Homo sapi AC024580 Homo sapi AF013613 Fugu rubr A28025 Human prepr	AZ8022 Hudian prepara AZ8023 Hudian prepara X12582 Bovine prep M13826 Ptg preprog AC092758 Papio cyn AF232689 Rat cytom M18102 Rat galanin J03624 Rat galanin AC007515 Homo sapi AC009821 Homo sapi	AC013458 Homo sapi AL1363800 Human DNA AC1136328 Mus muscu AF111168 Homo sapi AP004030 Oryza sat AP004070 Oryza sat AP004070 Oryza sat M89952 Bos taurus I18807 Sequence 1 M99057 Bovine nitr AC19052 Homo sapi AC09072 Homo sapi AC00972 Homo sapi AC03116 Mus muscu AP001038 Homo sapi AC034116 Mus muscu AP001732 Homo sapi AC034116 Mus muscu AP001732 Homo sapi AC02464 Homo sapi AC02464 Homo sapi AC02464 Homo sapi AC02464 Homo sapi AC02464 Homo sapi	PAT 01-MAY-2001 iata; Vertebrata; Euteleostomi; rrhini; Hominidae; Homo. ilbun,E., Zambrowicz,B. and polynucleotides encoding the same ;
· OI	AX11243 AX112343 AX112345 AF188492 AF188490 0 AF188491 AC023887 AC011506 AC011506 AC011506	A28025 A28025 I66494 BTGALAN PTGGAL AC092758 A AF23268 O RATGAL A AC07515 AC007515 AC007523	AC0109821 AC0109821 AC013980 AC012135 AMM1M10 AMM1M10 AMM04030 AP004030 BOVECNOS I18807 BOVNIOXSY CNSO6C7V AC090622 AC09072 AC09072 AP001732 AP001732 AP001733 HUMBTRO AC022642 AC022643 HUMCO02310	JIGNMENTS J127273. J127273. J127273. Ata; Craniata; tes; Catarrhin; ang,X., Hilbun, ang,X., Hilbun, ang,Ar.,
ue	426 351 347 947 947 974 104824 100110 200603	0.8 575 0.8 575 0.2 757 0.2 675 0.2 774 9.4 172896 9.3 129896 9.3 680 9.3 680 9.3 162060 9.2 172328		AX112343 426 bp DD N Sequence 1 from Patent WOO AX112343.1 GI:13939104 AX112343.1 GI:13939104 AMMENTO SAPIENS EUKATYOTA; METAZOA; ChOrd MAMMENTO SE 1 O 426) S TUTNET,C.A., Donoho,G., W. SANGA,A.T. HUMAN GALBAIN family prot. L Patent: WO 0127273-A 1 19 Lexicon Genetics Incorpor Location/Qualificities 1. 426 /Organism-"Homo
ult No. Score	2966 2966 2966 2966 1834 1556 1556	111 122 133 144 114 115 116 117 118 118 118 118 118 118 118 118 118	C 23 39.4 C 24 39.2 26 39.2 26 39.2 C 27 38.8 C 29 38.6 C 31 38.4 C 33 38.4 C 34 38.4 C 35 38.4 C 36 38 37.4 C 41 37.2 C 41 37.2 C 44 37.2	RESULT 1 AX112343 LOCUS LOCUS LOCUS LOCUS LOCUS LOCUS AX. ACCESION AX VERYWORD AX VERYWORD AX SOURCE ORGANISM HO BU BU AUTHORS TU JOURNAL PA FEATURES SOURCE LOCUS FEATURES SOURCE LOCUS FEATURES FEATURES SOURCE LOCUS FEATURES FEATURES SOURCE

```
Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local
                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                     RESULT
AF188492
                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDS
                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                       δŏ
                                          qq
                                                                δ
                                                                                   g
                                                                                                      δŏ
                                                                                                                         g
                                                                                                                                                                g
                                                                                                                                                                                     δŏ
                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human galanin family proteins and polynucleotides encoding the same Patent: WO 0127273-A 3 19-APR-2001; Lexicon Genetics Incorporated (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkamania; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 31)
Turner.C.A., Donoho,G., Wang,X., Hilbun,E., Zambrowicz,B. and
                                                                                                                                     actccagcatccgcacctgcccaccggggacgaggaggctggaccctcaatagtgctggc 120
                                                                                                                                                                                                                                                  ccacagocoteccaagaggaatgtgatggagacgtttgccaaaccagagattggaggtaaa 300
                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 atggetectecetecgtececetggtectectectectettgetggeggetgggagg 60
                                                                                                                                                                                                                                                                                      .
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                   Length 426;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6; Length 351;
                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                               100.0%; Score 426; DB 6; L
100.0%; Pred. No. 1.2e-104;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              PAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 296.4; DB 6
Pred. No. 1.3e-69;
0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ų
          72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        68
                                                                                                                                                                                                                                                                                                                                                                                                                                          AX112345 351 bp DNA
Sequence 3 from Patent WO0127273.
AX112345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9606"
115 c 91 g
           120 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX112345.1 GI:13939105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            69.68;
          127 c
                                                                  Matches 426; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 300; Conservative
                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
        107 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ø
                                                                                                                                                                                                                                                                                                                                                                       421 tcatag 426
                                                                                                                                                                                                                                                                                                                                                                                   421 TCATAG 426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human.
                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DEFINITION
                                                                                                                                                                                                                                                  241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                AX112345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                       g
                                                                                                                           δ
                                                                                                                                              qq
                                                                                                                                                                   ò
                                                                                                                                                                                     g
                                                                                                                                                                                                                            g
                                                                                                                                                                                                    -8
                                                                                                                                                                                                                                                 à
                                                                                                                                                                                                                                                                   셤
                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                               ò
                                                                                                                                                                                                                                                                                                                                                                     ò
```

ô

```
/translation="MAPPSVPLVLLLVLLSLAETPASAPAHRGRGGWTLNSAGYLLG
PVLHLPQMGDQDGKRETALEILDLWKAIDGLPYSHPPQPSKRNVMETFAKPEIGDLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 947)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ohtaki,T., Kumano,S., Ishibashi,Y., Oqi,K., Matsui,H., Harada,M., Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.
Isolation and CDNA cloning of a novel galanin-like peptide (GALP) Grom porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens clone pGR2HL14 galanin-like peptide precursor, mRNA, complete cds.
AF188492
                                 Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan Location/Qualifiers
                                                                                                                                                                                                                                                 1 ATGGCTCCTCCCTCCTCCTCCTCCTCCTCCTCTTGCTGAGCCTGGCAGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 9; Length 947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="neuropeptide"
/codon_start=1
/product=galanin-like peptide precursor"
/protein_id="AARF9724.1"
/db_xref="GI:6634714"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 69.6%; Score 296.4; DB 9 98.0%; Pred. No. 1.2e-69; iive 0; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 249 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               212 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="pGR2HL14"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 947)
Obtaki, T. and Kumano, S.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LSMKIPKEEDVLKS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF188492.1 GI:6634713
                                                                                                                                                                                                                                                                                                                                                                                                                                              947 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             240 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 300; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ø
                                                                                                                                                                                                                                                                                                                     301 gccagg 306
                                                                                                                                                                                                                                                                                                                                                         301 GGCATG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF188492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       g
```

δλ g δy qq ŏ q δ

```
/codon_start=1
/product="galanin-like peptide precursor"
/protein_id="AAF1972.1"
/protein_id="AAF1972.1"
/protein_id="MAIJ7DLIVLAVLLSLMESPASAPVHRGRGGWTLNSAGYLLGPV
/translation="WAIJTVPLIVLAVLLSLMESPASAPVHRGRGGWTLNSAGYLLGPV
LHPPSRAEGGGRGRTALGILDLWRAIDGLPYPOSQLASKRSLGETFAKPDSGVTFVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ohtaki, Kumano, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M., Kitada, C., Kurokawa, T., Onda, H. and Fujino, M. Isolation and cDMA cloning of a novel galanin-like peptide (GALP) J. Biol. Chem. 274 (52), 37041-37045 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
rodustries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    149 cccaaatgggtgaccaagacggaaagaggagacagccttgagatcctagacctgtgga 208
                                                                                                                                                Sus scrofa galanin-like peptide precursor, mRNA, complete cds. AF188490
143 ACTCCAGCATCCGCACCTGCCCACCGGGGACGAGGAGGCTGGACCCTCAATAGTGCTGGC 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       43.2%; Score 184.2; DB 4; Length 68.5%; Pred. No. 2.5e-39; tive 0; Mismatches 118; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                209 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Sus scrofa"
/db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="neuropeptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PDVVPWKRIRPGTTRFQI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                229 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Industries, Ltd., Wadai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and Kumano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF188490.1 GI:6634709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (bases 1 to 974)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 272; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohtaki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           258
                                                                                                                                                                                                                                                                                                                                                                    301 gccagg 306
                                                                                                                                                                                                                                                                                                                                                                                                                   . 383 GGCATG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AF188490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               염
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ŏλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δy
                                                                                                                                                                                                                                                                                                                     Оp
                                                                                                                                                                                                                                                                                                                                                                         ŏ
                                                                                                                                                                                                                      qq
                                                                                                                                                                       ŏ
                                                                         ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="MAPPSVPLVLLLVLLSLAETPASAPAHRGRGGWTLNSAGYLLG
PVLHLPQMGDQDGKRETALEILDLWKAIDGLPYSHPPQPSKRNVMETFAKPEIGDLGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 947)
Mohatai, T., Kumanov, S., Ishibashi, Y., Ogi, K., Matsui, H., Harada, M., Kitada, C., Kurokawa, T., Onda, H. and Fulino, M.
Isolation and cDNA cloning of a novel galanin-like peptide (GALP) J. Biol. Chem. 274 (52), 37041-37045 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens clone pGR2HL02 galanin-like peptide precursor, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
Industries, Ltd., Wadai 10, Tsukuba, Ibaraki 300-4293, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83 Argeorecoreconscience of the Argeorecas of th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 atggctcctccctccgtcccctggtcctcctcqtcctcttgctgactggcagag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                          121 taccttctgggtcccgtcctccaccttccccaaatgggtgaccaagacggaaaggggag 180
                                                                                                                                                                                                                              69.2%; Score 294.8; DB 9; Length 947; 97.7%; Pred. No. 3.1e-69; tive 0; Mismatches 7; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="galanin-like peptide precursor"
/protein_id="AAR19725.1"
/db_xref="G1:6634716"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="pGR2HL02"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="neuropeptide"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              212 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LSMKIPKEEDVLKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 947)
Ohtaki, T. and Kumano, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AF188493.1 GI:6634715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 97.77
Matches 299; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83. .433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . .947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                             301 gccagg 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               383 GGCATG 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AF188493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               qq
                                                                                                                                                                                                                                                                                                                                                                                                 q
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ď
```

Gaps

```
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                        AC023887
                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                      RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMMENT
                     οy
                                                 qq
                                                                                   δy
                                                                                                                    qq
                                                                                                                                                       ŏ
                                                                                                                                                                                    Db
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MACSKHLVLFLTILLSLAETPDSAPAHRGRGWTLNSAGYLLGP
VLHLSSRANGGRKTDSALEILDLWKAIDGLPYSRSPRMTKRSMGETFVKPRTGDLRIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohtaki,T., Kumano,S., Ishibashi,Y., Ogi,K., Matsui,H., Harada,M., Kitada,C., Kurokawa,T., Onda,H. and Fujino,M.
Isolation and CDNA cloning of a novel galanin-like peptide (GALP)
Trom porcine hypothalamus
J. Biol. Chem. 274 (52), 37041-37045 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus galanin-like peptide precursor, mRNA, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 (bases 1 to 694)
Ohtaki,T. and Kumano,S.
Direct Submission
Submitted (21-SEP-1999) Discovery Res. Labs. 1, Takeda Chemical
Industries, Ltd., Waddai 10, Tsukuba, Ibaraki 300-4293, Japan
Location/Qualifiers
177 CCTCCAGGGCTGAAGGAGGGGGAAGGGGAAGACACCCTCGGGATCCTGGACCTGTGGA 236
                                 209 aggccatcgatgggctccctactcccacctccacagcctccaagaggaatgtgatgg 268
                                                                237 AGGCCATTGATGGGCTCCCCTATCCCCAGTCTCAGTTGGCCTCCAAGAGGAGTCTGGGGG 296
                                                                                                  269 agacgitigccaaaccagagatiggaggiaaagccaggaaacacagaagagagacaccga 328
                                                                                                                                                                    329 caggagagagggaacaaggaagtggcaggcagagcttagaggatctggggcatgctcagca 388
                                                                                                                                  297 AGACTITCGCCAAACCAGACTCTGGAGTAACATTTGTTGGAGTTCCTGACGTGGTGCCGT 356
                                                                                                                                                                                         357 GGAAACGAATCCGACCAGGAACTACGAGG-----TITCAGATCTAGGCAAGCTCTGCA 409
                                                                                                                                                                                                                                                                                                                                                                    24-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 etcogtococctggtoctcotcotcottgctgagoctggagactccagcato 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 10; Length 694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
43.1%; Score 183.6; DB 10; Length (
Best Local Similarity 77.6%; Pred. No. 3.7e-39;
Matches 222; Conservative 0; Mismatches 64; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="galanin-like peptide precursor"
/protein_id="AAF19723.1"
/db_xref="G1:6634712"
                                                                                                                                                                                                                                                                                                                                                                   ROD
                                                                                                                                                                                                                                    389 tgaaaattcccaaggaaggaagatgtcctgaagtcata 425
                                                                                                                                                                                                                                                      /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:10116"
126. .473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="neuropeptide"
                                                                                                                                                                                                                                                                                                                                                               mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     143 g
                                                                                                                                                                                                                                                                                                                                                                                                                        AF188491.1 GI:6634711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKNVPDEEATLNL"
                                                                                                                                                                                                                                                                                                                                                          694 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 694)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   201 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Norway rat.
                                                                                                                                                                                                                                                                                                                                                          AF188491
                                                                                                                                                                                                                                                                                                                                                                                                          AF188491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 195
                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                    AF188491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                        RESULT
 g
                                   ð
                                                                g
                                                                                                   à
                                                                                                                                  g
                                                                                                                                                                                                q
                                                                                                                                                                    ð
                                                                                                                                                                                                                                    δ
                                                                                                                                                                                                                                                                  g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ŏ
```

```
Submitted (18-FEB-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                  132 tecegicetecaceticeceaaigggigaceaagaeggaaagggagaeagecetiga 191
                                                                                                  192 gatectagacetgtggaaggecategatgggetecectacteceaecetecacagecete 251
                                                                                                                                                                                                                                                                                                       17-AUG-2000
                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 19 clone RP11-541M19, WORKING DRAFT
SECUENCE, 8 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MO 63108, USA
On Aug 17, 2000 this sequence version replaced gi:7631054.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    arbitrary Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          * NOTE: This is a 'working draft' sequence. It currently consists of 8 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Center: Washington University Genome Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2092: contig of 2092 bp in length
2192: gap of unknown length
7044: contig of 4852 bp in length
7144: gap of unknown length
19499: contig of 12355 bp in length
19599: app of unknown length
3475: contig of 14876 bp in length
34575: gap of unknown length
                                                                                                                                                      ----- Genome Center ------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                                                                                                                                                           HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 164824)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 164824)
Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                        AC023887.4 GI:9838262
                                                                                                                                                                                                                                                                                             AC023887 164824 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center code: WUGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7145
19500
19600
34476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7045
                                                                                                                                                                                                                                                                                                                                                                                                                    Juman.
```

```
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC024580/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
           REFERENCE
                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                      TITLE
                                                                              COMMENT
                                                                                                                                                                                                                                                                                                      ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (07-OCT-1999) Production Sequencing Facility, DOE Joint
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

M. (Bases 1 to 100110)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens chromosome 19 clone CTD-2086L14, complete sequence. Ac011506.3 GI:7630361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 155.4; DB 2; Length 164824;
Pred. No. 1e-31;
0; Mismatches 6; Indels 0; 0
47285: contig of 12710 bp in length 47385: gap of unknown length 72270: contig of 24885 bp in length 72370: gap of unknown length 97221: contig of 24851 bp in length 97321: gap of unknown length 164824: contig of 67503 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    702 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="assembly_name:Contig16"
41699 c 42797 g 41321 t
                                                                                                                                                                                                                                             2193. 7044
/note="assembly_name:Contig10"
7145. 19499
/note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                             19600. 34475
/note="assembly_name:Contig12"
34576. 47285
                                                                                                                                                                                                                                                                                                                                                                   /note="assembly_name:Contig14"
                                                                                                                                                                                                                                                                                                                                       /note="assembly_name:Contig13"
                                                                                                                                                                                                                                                                                                                                                                                     72371. .97221
/note="assembly_name:Contig15
                                                                                                                                                                                                     /note="assembly_name:Contig9

    1. .164824
    /organism="Homo sapiens"
    /db_xref="taxon:9606"

                                                                                                                                                                     /clone="RP11-541M19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 100110)
DOE Joint Genome Institute.
                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                           vector_side:right"
                                                                                                                                                                                                                              vector_side:right"
                                                                                                                                                             /chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                          .164824
                                                                                                                                                                                                                                                                                                                                                                                                               clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          y Match
Local Similarity 96.4%;
hes 159; Conservative
                                                                                                                                                                                                                clone_end:T7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
                                                                                                                                                                                                                                                                                                                                                            47386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38305 a
                                     47386
72271
72371
        34576
47286
                                                                             97222
97322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                misc_feature
                                                                                                                                                                                                                                                                                                                                                             misc_feature
                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                               misc_feature
                                                                                                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                      misc_feature
                                                                                                                                                                                            misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AC011506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                            FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           οy
```

JOURNAL

```
Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA on Apr 20, 2001 this sequence version replaced gi:9954666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 100110)

DOE Joint Genome Institute and Stanford Human Genome Center.
                                                                                 Submitted (21-APR-2000) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Greek, CA 94598, USA on Apr 21, 2000 this sequence version replaced g1:6910529.

Draft Sequence Produced by DOE Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HTG 20-APR-200 DNA HTG 20-APR-200 HTG BRAFT HOME SAPIENS CHROMOSOME 19 CLONE CTD-2621117, WORKING DRAFT SEQUENCE, 51 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 9; Length 100110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                         www.jgi.doe.gov
Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                www-shgc.stanford.edu
Quality: Phrap Quality >-40 99.9% of Sequence:
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC24580.4 GI:13699641
HTG: HTGS_PHASE1; HTGS_DRAFT; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 36.1%; Score 153.8; DB 9; Best Local Similarity 95.8%; Pred. No. 2.8e-31; Matches 158; Conservative 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center Project Name: 836654, BC801678
Center clone name: CITB-E1_2621117
                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="CTD-2086L14"
26449 a 23149 c 22857 g 27655 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing of Human Chromosome 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.jgi.doe.gov
                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="19"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center: Joint Genome Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 200603)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 200603)
DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .100110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Project Information
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center Code: JGI
                                                                                                                                                                                                                                                                                                                   WI-11903 G21646.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AC024580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human.
```

```
Consensus quality: 157877 bases at least Q40
Consensus quality: 174287 bases at least Q30
Consensus quality: 174287 bases at least Q30
Consensus quality: 18024 bases at least Q30
Estimated insert size: 192390; agarose-fp estimation
Estimated insert size: 195603; sum-of-contigs estimation
Quality coverage: 5.09 in Q20 bases; sum-of-contigs estimation
* NOTE: This is a 'working draft' sequence: It currently
* consists of 51 contigs. The true order of the pieces
* arbitrary. Gaps between the content of the pieces
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                    1144: contig of 1144 bp in length
1244: gap of unknown length
3016: contig of 1772 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                        gap of unknown length
contig of 1110 bp in length
contig of 1124 bp in length
contig of 1124 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bp in length
length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        length
bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2038 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pb in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ength
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length
bp in 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gap of unknown len
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of unknown contig of 1663 gap of unknown contig of 1662 gap of unknown gap of unknown contig of 1200 gap of unknown contig of 1377 gap of unknown contig of 1691 gap of unknown contig of 1191 gap of unknown contig of 1191 gap of unknown contig of 1127 gap of unknown contig of 1224 bap of unknown contig of 1314 bap of unknown leaver and the same contig of 1314 bap of unknown leaver and the same contig of 1314 bap of unknown leaver and the same contig of 1314 bap of unknown leaver and unknown leave
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          contig of 1929 bgap of unknown l
contig of 1605 bgap of unknown l
contig of 1079 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  unknown
of 1747 h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              unknown ]
of 1289 b
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            contig of 2432
gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig of 1719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
of 1818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 1224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contiq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10846
Summary Statistics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               42875:
                                                                                                                                                                                                                                                                                                                                                                                          1245
                                                                                                                                                                                                                                                                                                                                                                       1145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5451
5551
6614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15834
15934
17377
17477
18668
18768
20045
20145
21369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14043
14143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22783
22883
24812
24912
26517
26517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27696
27796
30228
30328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32047
32147
333362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      33462
34686
34786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36533
36633
37922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38022
40060
40160
```

```
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 200603;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
contig of 2376 bp in length contig of 2376 bp in length contig of 1036 bp in length contig of 2404 bp in length contig of 1287 bp in length contig of 1287 bp in length contig of 1828 bp in length contig of 1828 bp in length contig of 1828 bp in length contig of 1952 bp in length contig of 2328 bp in length contig of 2328 bp in length contig of 3200 bp in length contig of 3200 bp in length contig of 3200 bp in length contig of 5239 bp in length contig of 5339 bp in length contig of 5330 bp in length co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5187 115286: gap of unknown length 5287 126142: contig of 10856 bp in length 126142: apa of unknown length 5243 140107: contig of 13865 bp in length 1108 140207: gap of unknown length 5268 150877: contig of 10670 bp in length 5978 150977: gap of unknown length 150977: gap of unknown length 150977: gap of unknown length 150978 150977: gap of unknown length 150978 150979: contig of 49626 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of unknown length contig of 12977 bp in length gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gap of unknown length contig of 3923 bp in length gap of unknown length contig of 4418 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5014 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="calTech human BAC library D" 46306 a 50919 c 51731 9 46633 t 5014 other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF013613 28199 bp DNA
Fugu rubripes cosmid 48D10, complete sequence.
AF013613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.8%; Score 88.4; DB 2; 98.9%; Pred. No. 1.3e-13; iive 0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /chromosome="19"
/clone="CTD-2621117"
                                                                                                                                                                                                                                         54124:
54224:
                                                                                                          18405:
                                                                                                                                                                                      52196:
                                                                                                                                                                                                                  52296:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89856:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                84446:
                                                                                                                                                                                                                                                                                              57287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 98.99
Matches 89; Conservative
                                                                                                                           48406
50810
50910
52197
                                                                                                                                                                                                                                                               54125
54225
57288
57388
59340
59440
62168
62268
65533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68833
68933
73579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79008
79108
84347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89757
89857
93569
93669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140108
140208
150878
150978
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCUS
DEFINITION
ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF013613/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT
```

ö

```
Comparative analysis of the polycystic kidney disease 1 (PKD1) gene reveals an integral membrane glycoprotein with multiple evolutionary conserved domains
Hum. Mol. Genet. 6 (9), 1483-1489 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (11-JUL-1997) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA On Nov 21, 1997 this sequence version replaced gi:2623547. Submitted by:
                                                                           Eukarrota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthomorpha; Acanthomorpha; Percomorpha; Tetraodontiformes; Tetraodontidae; Takifugu.
                                                                                                                                                                                                              Sandford, R., Sqotto, B., Aparicio, S., Brenner, S., Vaudin, M., Wilson, R., Chissoe, S., Pepin, K., Bateman, A., Chothia, C., Hughes, J. and Harris, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Washington University Genome Sequencing Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Fugu rubripes Genome Sequencing Project Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The sequence of Fugu rubripes 48D10
                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 28199)
Hawkins, J. and Gillam, B.
AF013613.1 GI:2627437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (1997)
3 (bases 1 to 28199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 28199)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
                                                 Takifugu rubripes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Waterston, R.
                                                                                                                                                                                                                                                                                                                                                                                                   97449170
                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
  VERSION
KEYWORDS
                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
```

NOTICE: This sequence may not be the entire insert of this clone. It may be shorter because we only sequence overlapping sections once, or longer because we provide a small overlap between neighboring submissions.

Washington University,

Department of Genetics, Washii St. Louis, MO 63108, USA e-mail: rw@nematode.wustl.edu

Genome Sequencing Center

all regions were double stranded or sequenced with an alternate chemistry; an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by This sequence was finished as follows unless otherwise noted: sequence from more than one subclone

Library information: Gridded Fugu library from the UK HGMP Resource Centre at Hinxton.

NEIGHBORING COSMID INFORMATION:

The left neighbor is 259C6, 19100 base overlap. The actual start of this clone is at base position 22192 of 259C6; the actual end is at base position 28199 of 48D10.

This cosmid contains a tandem repeat from 23145 to 25326. The tandem is deleted, and has regions which are single stranded. Attempts to size the deletion with digest data were inconclusive. The size was estimated to be 1.7 kb from a PCR product obtained by Dr. Dick Sandford.

Coding sequences below are predicted from computer analysis, using the program Genefinder(P. Green and L. Hillier, ms in preparation).

Location/Qualifiers
1. .28199

/organism="Takifugu rubripes"

source

FEATURES

```
/product="galanin"
/product="galanin"
/protein_id="CAA01907.1"
/db_xref="G1:1247490"
/trans_lation="MARGSALLASLLLAAALSASAGLWSPAKEKRGWTLNSAGYLLG
PHAVGNHRSFSDKNGLTSKRELRPEDDWKPGSFDRSIPENNIMRTIIEFLSFLHLKEA
                                                                                                                                                                                                                                             /-evidence=not_experimental
/protein_id="AABB6684.1"
/db_xref="61:2627438"
/db_xref="61:2627438"
/db_xref="61:2627438"
/db_xref="61:2627438"
svpFqGSSALLTAVIXITVEVGLTGNTLAITVERAGMETYNIXITIMANDBENGSTG
SVPFGGSSALLTAVIXITYEVELGYNATADSNNQFTSIFCLTVMSIDRYLAVVPIRE
IVGGLFGLAFQNVSAAVMAVGSFVVVLPVVIFSDVQVRPSRPLQVGTSSKCLVKRVQETF
NSCNMIMPERAKVVSAAVMAVGSFVVVLPVVIFSDVQVRPSRPLQVGTSSKCLVKRVQETF
NSCNMIMPERAKVVSAAVMAVGSFVVVLPVVIFSDVQVRPSRPLQVGTSCLVKRVQETF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HUMAN GALANIN, CDNA CLONES ENCODING HUMAN GALANIN AND A METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Db 24960 AAGAGAGACTGAGAGAGAGAGAGAGAGAAGAGAGAATTGAGGGAGAGAGAGAGAGAG 24901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               253 aagaagaatgtgatggagacgtttgccaaaccagagattggaggtaaagccaggaaacac 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-SEP-1995
                                                                                                                   26058. .28156
//gene="F-48010.1"
join(26058. .26702,27932. .28156)
/gene="F-48010.1"
/note="Belongs to family 1 of G-protein coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 47; DB 5; Length 28199;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 46; DB 6; Length 575; Pred. No. 0.059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAT
                                                                                        /note="tandem with deletion"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRODUCING HUMAN GALANIN
Patent: WO 9215681-A 5 17-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A28025 575 bp DNA
Human preprogalanin CDNA sequence.
A28025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1. .575
/organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GALDRILDIPAAASSEDIERS
/db_xref="taxon:31033"
/chromosome="UL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                   6389 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                     /codon_start=1
                                     /clone="48D10"
                                                           /map="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                STCPLNICCLSRR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10.8%;
59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11.0%;
62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A28025.1 GI:1247489
                                                                                                                                                                                                                  receptors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 575)
                                                                                                                                                                                                                                                                                                                                                                                                                                     6758 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 62.2
Matches 74; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numan.
                                                                                  repeat_region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                         gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURES
                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A28025
```

```
Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                         qalanin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE
                                                                                                                                                                                                                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
                                                                                                                                                                                                                                                                                                                                               BTGALAN
                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                       g
                                                                                                                               QY
                                                                                                                                                    qq
                                                                                                                                                                              δy
                                                                                                                                                                                                   qq
                                                                                                                                                                                                                           δλ
                                                                                                                                                                                                                                                 QQ
        ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ò
                                                                                                                                                                                                                                                                                    Unclassified.

1 (bases 1 to 575)

Evans, H.Frances and Shine, J.

Human galanin, CDNA clones encoding human galanin and a method of producing human galanin

Patent: US 5756460-A 8 26-MAY-1998;
                                                                      61 actccagcatccgcacctgcccaccggggacgaggaggctggaccctcaatagtgctggc 120
       Gaps
                                                                                     14 ArGGCCCGAGCGCCTCCTCCTCCTCCTCCTCCTCGCCGGCCCTTTCTGCC 73
                                                                                                                                                                                                             04-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 atggctcctccctccgtccccctggtcctcctcctcgtccttgctgagcctggcagag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14 Aridecceangearaccercerecrecercerecreceseseseseses 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-DEC-1997
       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 6; Length 575;
      55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 6; Length 575
Pred. No. 0.059;
0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           368 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 7218)
Dorner,F., Scheiflinger,F. and Falkner,F.Gunter.
Recombinant fowlpox virus
Patent: US 5670367-A 14 23-SEP-1997;
Location/Qualifiers
1. .7218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PAT
   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1929 t
                                                                                                                                                                                                   Sequence 8 from patent US 5756460.
AR009787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100494 7218 bp DNA
Sequence 14 from patent US 5670367.
166494
                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
1. .575
                                                                                                                                                                                                                                                                                                                                                                                     /organism="unknown"
162 c 140 a
                                                                                                                                                                                                                                                                                                                                                                                                140 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="unknown"
1491 c 1486 g
                                                                                                                                                                                                                                          AR009787.1 GI:3968592
                                                                                                                                                                                                                                                                                                                                                                                                                                               10.8%;
59.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GI:2724471
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79; Conservative
                                                                                                                     121 taccttctgggtcc 134
                                                                                                                                            134 TACCTGCTGGCCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 taccttctgggtcc 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               134 TACCTGCTGGGCCC 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unclassified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                               128 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1944 a
                                                                                                                                                                                                                                                                Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           I66494.1
                                                                                                                                                                                                                                                                               Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unknown.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Unknown
79;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                        source
                                                                                                                                                                                                                 DEFINITION
                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
  Matches
                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 13
                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                            AR009787
                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166494/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KEYWORDS
                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE
                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGIN
                                                                      δ
                                                                                             g
                                                                                                                     å
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
```

```
ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MPRGSVLLLASLLLAAALSATLGLGSPVKEKRGWTLNSACYLLG
PHALDSHRSFQDKHGLAGKRELEPEDEARPGSFDRPLAENNVRTIIEFLFFLHLKDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bovidae; Bovinae; Detarclodactyla; Ruminantia; Pecora; Bovoldea; 1 (bases 1 to 675)
Rokaeus, A. and Carlquist, M. Nucleotide sequence analysis of CDNAs encoding a bovine galanin precursor protein in the adrenal medulla and chemical isolation of BDS Lett. 234 (2), 400-406 (1988)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovoidea,
                                                                                                                                  152 aaatgggtgaccaagacggaaagagggagacagccttgagatcctagacctgtggaagg 211
                                                                                                                                                                              212 ccatcgatgggctcccctactcccacctccacagccctccaagaggaatgtgatggaga 271
                                                                                                                                                                                                                                                                    272 cgtttgccaaaccagagattggaggtaaagccaggaaacacagaagagagacaccgacag 331
                                                                                                                                                                                                                                                                                                                                                        332 gagaggggaacaaggaagtggcaggcagacttagaggatctgggcatgctcagcatga 391
                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                     ö
         DB 6; Length 7218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 675;
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    148. .243
/product="signal peptide (AA -32 to -1)"
148. .519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /product="preprogalanin (AA -32 to 91)"
/protein_id="CAA31094.1"
/db_xref="G1:377"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /cell_type="adrenal chromaffin cells"
/clone="bGAL 1.21, bGAL 4.81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MAM
                                                     98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244. .330
/product="galanin (AA 1 - 29)"
253 c 188 g 111 t
Query Match 10.7%; Score 45.4; DB Best Local Similarity 1.5%; Pred. No. 0.07; Matches 4; Conservative 167; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 10.2%; Score 43.4; DB Best Local Similarity 54.8%; Pred. No. 0.29; Matches 86; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="SWISS-PROT:P11242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1087 RRRRRRRRRRRRRRRRRRATCGCAAG 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                392 aaattcccaaggaggaagatgtcctgaag 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1. 675
/organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GALERLPSIPTAESAEDAERS"
244. 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    188 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bovine preprogalanin mRNA.
X12582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X12582.1 GI:376
```

```
ö
                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. (pases 1 to 774)

Roekaeus, A. and Brownstein, M.J. Construction of a porcine adrenal medullary cDNA library and nucleotide sequence analysis of two clones encoding a galanin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12 ctccgtccccctggtcctcctcctcgtccttgctgagcctggcagagactccagcatc 71
27-APR-1993
                                                                                                                                                                                                                                                         Pig adrenal gland, cDNA to mRNA, clones pGAL5A2, pGAL8B2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match

9.7%; Score 41.4; DB 4; Length 774;
Best Local Similarity 58.5%; Pred. No. 1;
Matches 72; Conservative 0; Mismatches 51; Indels
                                                                                                                                                                                                                                                                                                                                                               Proc. Natl. Acad. Sci. U.S.A. 83, 6287-6291 (1986)
86313566
                                                                                                                                                                                              MAM
                                                                                                      132 tecegteetecacettececaaatgggtgaccaagae 168
                                                                                                                              279 ACCACATGCGCTCGACAGCCACAGGTCATTCAAGAC 315
                                                                                                                                                                                   PIGPGAL 774 bp mRNA
Pig preprogalanin mRNA, complete cds.
M13826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    130 t
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="preprogalanin"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="galanin"
281 c 222 g
                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                        .599
                                                                                                                                                                                                                                    M13826.1 GI:164605
                                                                                                                                                                                                                                                                              Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       141 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 tcc 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     359 GCC 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             mat_peptide
                                                                                                                                                                                                           DEFINITION
ACCESSION
                                                                                                                                                                                                                                                   KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                JOURNAL
MEDLINE
                                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                      PIGPGAL
                                                                                                                                                                                                                                                                                                                                            TITLE
                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δλ
                                                                                   g
                                                                                                            δy
                               QQ
                                                           δλ
```

Search completed: March 2, 2002, 23:54:07 Job time: 10606 sec

		,
	,	 •

```
March 2, 2002, 20:31:41; Search time 1494.43 Seconds (without alignments) 3063.176 Million cell updates/sec
                                                                                                                                                                                                        426
1 atggetectecetecgtece.....aagatgteetgaagteatag 426
                                                                                                                                                                                                                                                                                                                                                  22703874
GenCore version 4.5 copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                           11351937 seqs, 5372889281 residues
                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                           IDENTITY_NUC Gapoxt 1.0
                                                                                                                                                                                                                                                                                                                                                                                         Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        em_estfun:*
em_esthum:*
em_estin:*
em_estom:*
                                                                                                                                                                                     US-09-689-911-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ESI:*
                                                                                                                                                                                                            Perfect score:
                                                                                                                                                                                                                                                               Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Database :
                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                              Sequence:
                                                                                                                  Run on:
                                                                                                                                                                                         Title:
```

5: em_estpl:*
6: em_estba:*
7: em_estco:*
8: em_estco:*
8: em_estco:*
10: gb_est:*
11: gb_htc:*
13: gb_htc:*
13: gb_htc:*
14: em_gss_inv:*
15: em_gss_inv:*
16: em_gss_roi*:
17: em_gss_roi*:
18: em_gss_roi*:
19: em_gss_roi*:
10: em_gss_roi*:
10: em_gss_roi*:
11: em_gss_roi*:
12: em_gss_roi*:
13: em_gss_roi*:
14: em_gss_roi*:
15: em_gss_roi*:
16: em_gss_roi*:
17: em_gss_roi*:
18: em_gss_roi*:
18: em_gss_roi*:
19: em_gss_roi*:
10: em_gss_roi*:
10: em_gss_roi*:
10: em_gss_roi*:
11: em_gss_roi*:
12: em_gss_roi*:
13: em_gss_roi*:
14: em_gss_roi*:
15: em_gss_roi*:
16: em_gss_roi*:
17: em_gss_roi*:
18: em_gss_roi*:
18: em_gss_roi*:
19: em_gss_roi*:
10: em_gss_roi*:
10:

		Description	AQ549952 RPCI-11-4	AW416677 52226 MAR	AW436648 77047 MAR	AL556408 AL556408	AL556409 AL556409	BI255627 602976496	AL504892 AL504892	BE060480 HVSME9001	BG176001 602335226	AV836850 AV836850		ALDUCAL # ALDUCAL #	AL065856 Drosopnii
SUMMARIES		ID	A0549952	AW416677	AW436648	AL556408	AL556409	BT255627	AL504892	BE060480	BG176001	AV836850	2000011	AL5021/4	CNS006S5
		DB	13	10	10	10	10	- 1	10	10	; ;	1 -	9 6	10	13
		Query Match Length DB	565	465	304	727	804	760	499	712	034		7	541	916
	æ	Query Match	35.4	0.00	200	10.0	8.01	201	. 0	. 0	10	000	0	8.6	9.8
		Score	150 6	123.6	0.00		•	* * *		4.04	10	0	0.14	41.6	41.6
		ъ.	-	10	۹ ۳	, =	* L	י ר	۰ د	- a		ח כ	5	_	7
		Result No.	1			,	נ				,	ບ່	U	0	S

Location/Qualifiers

FEATURES

BF254655 HVSMEf000	W83304 mf24d03.rl	W75493 me55b12.rl	AI894042 mg89g12.y	A2753635 RPCI-24-1	AL513663 AL513663			BF551196 UI-R-CO-h			AA016654 mg89g12.r		AL060767 Drosophil	AL108238 Drosophil	AK019070 Mus muscu	AQ937099 NBI-607R	BE403648 WHE0435_A	AL187533 Tetraodon	AW175662 RC3-BT004	AL056652 Drosophil	BE967163 601661043	ø			0		BF680503 602155222	_		Ω	AT.277084 Tetraodon	
BF254655) AL513663							_		3 CNS017MS										13 CNS00462								
999					481																			902								
8	7	. 0			, , ,	י י י	, o		. "			0	2.6	9.5	6.5	6.8	6	6	000	α	α			. 00	9	9.8	8	α				۵. ۵
41.6	41.2	1.5	2.1.4	7.7	* 0	9.0		. 0	0.00		4.00	. 6	0.00	66	60.6	300	0 00	37 8	37.6	37.6		0.70	27.0	3.7	36.8	36.8						
. 13) 	+ L	CT -) T	D C	. C	9 6	77	4 6	70		2,00			000		9 6			27			37	a c	0 6		7		7 7		45

ALIGNMENTS

RESULT 1 AQ549952 LOCUS DEFINITION ACCESSION VERYORDS SOUGANISM REFERENCE AUTHORS TITLE JOURNAL COMMENT

```
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 (bases 1 to 465)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Design and use of two pooled tissue normalized cDNA libraries for STA discovery in swine Unpublished (2000) Contact: Smith TPL
                                                                                                                          /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCI11 Human Male BAC Library"
1 144 c 142 g 144 t
                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-JUL-2000
                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                     DB 13; Length 565;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52226 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                          Query Match 35.4%; Score 150.6; DB 13; Best Local Similarity 94.5%; Pred. No. 2.6e-26; Matches 156; Conservative 0; Mismatches 9;

    .565
/organism="Homo sapiens"

                                                 /db_xref="taxon:9606"
/clone="RPCI-11-418L8"
/clone_lib="RPCI-11"
/sex="Male"
                                   /db_xref="GDB:7660399"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 24 row: B column: 13
Seq primer: ATTTAGGTGACATARG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW416677.1 GI:6944559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    465 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW416677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW416677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                   BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
AW416677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      õ
```

; 0

```
.;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 to 304)
Fabrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980994.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000) contact: Smith FPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pcMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." 92 g 56 t
                                                                                                                                                                                                          Gaps
                                                                                                                                      29 tcctcctcgtcctcttgctgagcctggcagagactccagcatccgcacctgccaccgg 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUL-2000
                                                                                                          ö
                                                                       DB 10; Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW436648 304 bp mRNA EST
77047 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
AW436648
                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
TEL: 402 762 4366
Fax: 402 762 4390
                                                                                                          44;
                                                                    Score 123.6; DB
Pred. No. 8e-20;
0; Mismatches
   6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plate: 32 row: F column: 8 Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .304
/organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="pooled"
/lab_host="DH10B"
     6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BACKWARD: GTTTTCCCAGTCACGACG
   133
                                                                    29.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AW436648.1 GI:6971954
 155 c
                                                                                                   Matches 150; Conservative
                                                                                                                                                                                                                                                                                                                                                     209 aggccatcgatggg 222
                                                                                                                                                                                                                                                                                                                                                                                      274 AGGCCATTGGTGAG 287
                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PCR PRimers
     σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sus scrofa
 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
                                                                      Query Match
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW436648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                               οy
                                                                                                                                                                                                                                                                                                                  QQ
                                                                                                                                                                                                                                                                                                                                                     ò
                                                                                                                                                                                                                                                                                                                                                                                  셤
```

Score 99.2; DB 10; Length 304; Pred. No. 5.5e-14;

23.3%; 76.2%;

Query Match Best Local Similarity

/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."

/clone_lib="MARC 2PIG" /tissue_type="pooled" /lab_host="DH10B"

```
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CscDoxO04YA08"
/clone="CscDoxO04YA08"
/clone="TscDoxO04YA08"
/clone="Tr_INFLO06_PL2"
/rissue_type="placenta"
/note="Vector: pCMVSPORT 6; Site_1: NotI; lst strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was digested with Not I and
enriched, double-stranded cDNA was constructed by
ucctor. Library was normalized by
Life Technologies. Contact : Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Fmail: fliangth.invitrogen.com"
http://tullength.invitrogen.com"

74 a 261 c 211 g 156 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordate; Catarrhini; Hominidae; Homo.
1 (bases 1 to 760)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI255627 760 bp mRNA EST 17-JUL-2001
602976496F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5115887 5',
                                                                                                                                                                    Homo sapiens

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.

1 (bases 1 to 804)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Thi,W.B., Albiraries and normalization

Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 actccagcatccgcacctgcccaccggggacgagggggggctggacctcaatagtgctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALS56409 804 bp mRNA EST 16-FEB-2001
ALS56409 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK004YA08 S
                                                                                                                                                                                                                                                                                                                                Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10.8%; Score 46; DB 10; Length 804; 59.0%; Pred. No. 0.45; tive 0; Mismatches 55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI255627.1 GI:14809207
                                                                                                                  AL556409.1 GI:12899058
                                                                    prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 taccttctgggtcc 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            347 TACCTGCTGGCCC 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
BI255627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sest Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 174 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
                                                                                                                                                                human.
                                                                                                                                          EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                 ORGANISM
                                                           DEFINITION
                                                                                                                                                                                                                                          REFERENCE
AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI255627
                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                     ACCESSION
                                                                                                                        VERSION
KEYWORDS
RESULT
AL556409
                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Op
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             499 ATGGCCCGAGGCAGCGCCTCCTCGCTCCTCCTCGCCGCCGGCCCTTTCTGCC 440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 atggctcctccctcgtcccctggtcctcctcgtccttgctgagcctggagag 60
                                                                                                                                                                                                                                                                                                                                                      ALS56408 727 bp mRNA EST 16-FEB-2001
ALS56408 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK004YA08 3
                                                                                                                        145 regircirgeagrecigereageergargaagrerecageereregerecages 204
      0; Gaps
                                           29 tectectegtectettgetgageetggeagagetecageateegeaeetgeeeaeggg 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: venoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Craniata; Vertebrata; Butele Libaess 1 to 727).
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10.8%; Score 46; DB 10; Length 727; 59.0%; Pred. No. 0.44; tive 0; Mismatches 55; Indels
      38; Indels
                                                                                                                                                                                                              149 cccaaatgggtgaccaagacggaaagagggagacagcct 188
                                                                                                                                                                                                                                    265 CCTCCAGGGCTGAAGGAGGGGAAGACACCCT 304
        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                AL556408.1 GI:12899056
                                                                                                                                                                                                                                                                                                                                                                                                           prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.8%
Best Local Similarity 59.0%
Matches 79; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              379 TACCTGCTGGCCC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 taccttctgggtcc 134
             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                 AL556408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              human.
               Matches 122;
```

source

FEATURES

DEFINITION

ACCESSION

KEYWORDS

SOURCE

VERSION

AL556408/c

RESULT

q οy qq

οχ

ORGANISM

AUTHORS JOURNAL

TITLE COMMENT

REFERENCE

BASE COUNT

ORIGIN

a δλ a â

Gaps

ö

```
;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
: Triticeae; Hordeum.
: Thitosae; Hordeum.
: Nases 1 to 499)
Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A.
EST sequencing and analysis in barley
                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Organ: cervix, Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.4 kb. Library prepared by Life
Technologis."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalek@ipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: T3 primer for 5'end.
                                                                                 CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11281 row: o column: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AL504892 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone Narchagos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          165 ATGGCCCGAGGCAGCCCTCCTTCTCGCCTCCTCCTCCTCGCCGCGCCCTTTCTGCC 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 actccagcatccgcacctgcccaccggggacgaggaggaggctggacctcaatagtgctggc 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                225 TCTGCGGGGCTCTGGTCGCCGGCCAAGGAAAACGAGGCTGGACCCTGAACAGCGGGGGC 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 atggetectecetecgtecectggtectectectegtecttgetgageetggeagag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10.4%; Score 44.4; DB 11; Length 760; 58.2%; Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:5115887"
/clone_lib="NIH_MGC_12"
/tissue_type="cervical carcinoma cell line"
/lab_host="bH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Hordeum vulgare"
                  Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                     High quality sequence stop: 645.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:9606
                                                                   Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AL504892
AL504892.1 GI:12031107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 58.20,
-Local 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               499 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Michalek W
  Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 285 TACCTGCTGGGCCC 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 taccttctgggtcc 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL504892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         barley.
                                                                                                                                                                                                                                                                                  source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL504892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     λο
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ò
```

/cultivar="Barke" /db_xref="taxon:4513" /clone="HW06L10V"

```
/note="Vector: Diasmid pBk-CMV; Site_1: ECORI; Site_2:
XhoI; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature Cloning
Sites: ECORI (5'-end of CDNA) and XhoI (3'-end of CDNA).
NOTE: Due to a cloning artefact caused by the kit, in most
cases the ECORI site is NOT present, as well as the ECORI
adapter. Average insert size is 1 kb Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'-and 3'-end until a 50 bp window contains less than two
ambiguities. The maximum length was set to 700 bp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
'Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo
'T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wood,T.
Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                42 TTGGTTTTGTCGCCGCCGTGCTCCTCGCCGTCCTCATGCCGGCCCTCGCCGCC 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62 eteccageatecgeacetgeceaceggggaegaggaggetggaeeeteaatagtgetgget 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BE060480 712 bp mRNA EST 29-MAY-2001
HVSMEG0012G18f Hordeum vulgare pre-anthesis spike EST library
HVCDNA0008 (white to yellow anther) Hordeum vulgare cDNA clone
HVSMEG0012G18f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for barley genomics
Unpublished (2000)
On Jun 9, 2000 this sequence version replaced gi:8405130.
                                                                                                                                                                                                                                                                                                                                                                                                                                             9.9%; Score 42.2; DB 10; Length 499; 56.6%; Pred. No. 3.3; tilve 0; Mismatches 59; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
/clone_lib="Hordeum vulgare Barke roots"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Hordeum vulgare"
/cultivar="Morex"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence start: 3
High quality sequence stop: 470.
                          /tissue_type="roots"
/lab_host="XLOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE060480.2 GI:13154317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (bases 1 to 712)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 accttctgggtcccgt 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 ACCTTCTGATGATCGT 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE060480
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 77;
                                                                                                                                                                                                                                                                                                                                            BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE060480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURES
                                                                                                                                                                                                                                                                                                                                                                    ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δλ
```

```
BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
AV836850/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                     258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                         q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                οy
                                                                                                                                                                                                                                                                                        g
                                                                                                                                                                                                                                                                                                                              à
                                                                                                                                                                                                                                                                                                                                                                 g
                                                                                                                                                                                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                     δ
                                                                                                                                                                            δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 602335226F2 NCI_CGAP_Mam1 Mus musculus cDNA clone IMAGE:4458199 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1: Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Gibbert Smith, NIH"
                                                                               /note="vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders"

200 c 186 g 179 t lothers
                                                                                                                                                                                                                                                                        ő
       /clone_lib="Mordeum vulgare pre-anthesis spike EST library HVcDNAN0008 (white to yellow anther)" /tissue_type="pre-anthesis spike" /lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NIH. WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                            62 ctccagcatccgcacctgcccaccggggacgaggaggatggacctcaatagtgctggct 121
                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-FEB-2001
                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                         DB 10; Length 712;
                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:4458199"
/clone_lib="NCI_CGAP_Mam1"
/tissue_type="tumor, biopsy sample"
/dev_stage="3 months, virgin"
/lab_host="DH10B"
                                                                                                                                                                                                                                         9.9%; Score 42.2; DB 56.6%; Pred. No. 3.6; tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          High quality sequence stop: 754.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="HVSMEg0012G18f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /strain="FVB/N"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG176001.1 GI:12682704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       934 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 accttctgggtcccgt 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            196 ACCTTCTGATGATCGT 211
                                                                                                                                                                                                                                                                                  77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG176001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BG176001
                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BG176001/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JOURNAL
COMMENT
                                                                                                                                                                      BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              g
                                                                                                                                                                                                                                                                                                                                                                                                                                       qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                   ŏ
```

```
Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="K. Sato unpublished cDNA library: Hordeum vulgare subsp. vulgare seedling leaves second leaf stage" /tissue_type="seedling leaves" /tissue_type="seedling leaves" | figure | 129 g | 62 t
                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV836850 420 bp mRNA EST 22-JUN-2001
AV836850 K. Sato unpublished cDNA library: Hordeum vulgare subsp.
vulgare seedling leaves second leaf stage Hordeum vulgare subsp.
vulgare cDNA clone rbasd27m22, mRNA sequence.
AV836850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637 GCAGACGGGAAGACAGGAAAGCAGAATGGAAGGCTGACCCAGGGACAGCAACATCCCAAG 578
                                                                                                                                                                                                                                                                                                                                                                    757 CCACCAGCAGAGCCACATTCAAGGCTCACACACAAAAGACCAGCGCACGTGACGTCAC 698
                                                                                                                                                                                                                                                                                                                                                                                                                                                      gaatgtgatggagacgtttgccaaaccagagattggaggtaaagccaggaaacacagaag 317
                                                                                                                                                                                                                                                                                                                                                                                                                          198 agacctgtggaaggccatcgatgggctcccctactcccacctccacagcctccaaagag 257
                                                                                                                                                                                                      78 tgcccaccggggacgaggaggctggaccctcaatagtgctggctaccttctgggtcccgt 137
                                                                                                                                                                                                                                                           817 CGGCCAACTICAATCAGAGGACGCAGICACACAAGACTCCGTGTGGAAACCTGCGGCCCCA 758
                                                                                                                                                                                                                                                                                                                 138 cctccaccttccccaaatgggtgaccaagacggaaagagggagacagcccttgagatcct 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: kassato@tib.okayama "u.ac.jp",
URL:http://www.rib.okayama "u.ac.jp/barley/
Sato, K., Saisho, D., Takeda, K., Shini, T. and Kohara, Y. Direct submission;
                                                                                                                                             22-JUN-2001
                                                                                                18 ececitygiceiceiceitegiceitygeigageeiggeagagiceageateegeaee 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     database:http://www.shigen.nig.ac.jp/barley/Barley.html.
Location/Qualifiers
                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barley EST sequencing project in NIG and Okayama Univ Unpublished (2001)
Contact: Kazuhiro Sato Research Institute for Bioresources Okayama University, Barley Germplasm Center Chuo 2-20-1, Kurashiki, Okayama 710-0046, Japan
Length 934;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Hordeum vulgare subsp. vulgare"
                                                  Indels
  DB 11;
                                                  0; Mismatches 177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:112509"
  9.8%; Score 41.8;
45.5%; Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar-"Haruna Nijo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone="rbasd27m22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 agagacaccgacaggagggggaa 342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       577 CAAGCCACCTGCAGGTGCTTCTGAA 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AV836850.1 GI:14528939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (bases 1 to 420)
        Query Match
Best Local Similarity 45.55
Matches 148; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 118 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sato, K.
```

Score 41.6; DB 10; Length 420;

9.88;

Query Match

BASE COUNT

```
/note="Nector: plasmid pBR-CMV; Site_1: EcoRI; Site_2:
Xho1; mRNA was made from roots of spring barley variety
'Barke', a high quality malting variety. Roots were grown
for two days on filter paper at room temperature Cloning
sites: EcoRI (5'-end of CDNA) and XhoI (3'-end of CDNA)
NOTE: Due to a cloning artefact caused by the kit, in most
cases the EcoRI site is NOT present, as well as the EcoRI
adapter. Average insert size is 1 kb Sequence trimming:
Vector sequences and sequence ends were trimmed from the
5'-and 3'-end until a 50 bp window contains less than two
ambiguities: The maximum length was set to 700 bp"
                                  ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Institute for Plant Genetics and Crop Plant Research
Corrensstr.3, D-06466 Gatersleben, Germany
Email: michalekeipk-gatersleben.de, http://pgrc.ipk-gatersleben.de
Seq primer: M13unj primer for 3'end.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó;
                                                                                                                                                                                                                                                                                                                                                                                      AL502174 Hordeum vulgare Barke roots Hordeum vulgare cDNA clone
HW06L1043', mRNA sequence.
                                                                                                       357 Traditirarcaccaccaracracracracaccarcercaraccaccaracaccacca 298
                                                                                                                                                   62 ctecagcatecgcacetgcccaceggggacgaggaggetggaceteaatagtgetgget 121
                                                                                                                                                                                           2 tggctcctccctccgtccccctggtcctcctcctcctcttgctgagcctggcagaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             458 TIGGITITGECCCGCCGCGCGCGCTCCTCGCCGTCCTCATGCCGGCCCTCGCCGCG 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 ctccagcatccgcacctgcccaccggggacgaggaggctggaccctcaatagtgctggct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 tggctcctccctccgtccccttggtcctcctcctcgtccttgctgagcctggcagaga 61
                                  ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Michalek,W., Weschke,W., Pleissner,K.-P. and Graner,A. EST sequencing and analysis in barley Unpublished (2000)
Contact: Michalek W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9.8%; Score 41.6; DB 10; Length 541;
56.6%; Pred. No. 4.8;
iive 0; Mismatches 59; Indels 0;
                              59; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Hordeum vulgare Barke roots"
/tissue_type="roots"
/lab_host="XLOLR"
         Pred. No. 4.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="HW06L10u"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Barke"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL502174.1 GI:12028389
56.6%;
                         77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 541)
                                                                                                                                                                                                                                                                                  237 ACCTTCTGATGATCGT 222
                                                                                                                                                                                                                                           122 accttctgggtcccgt 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hordeum vulgare
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Sim:
Matches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                               RESULT 11
AL502174/c
                                                                                                                                                                                                                                                                                                                                                                                                               DEFINITION
                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGIN
                                                                                                       QΩ
                                                                ŏ
                                                                                                                                                   ολ
                                                                                                                                                                                             Op
                                                                                                                                                                                                                                                                                QQ
                                                                                                                                                                                                                                         δ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ŏ
```

```
Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14709 of RPCI-98 library from Drosophila melanogaster (fruit AL065856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64 ccagcatccgcacctgcccaccggggacgaggaggctggaccctcaatagtgctggctac 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            829 SSAVASASSASSSVVAVSRSSVASASSVSBVASMSSRSVVCRRSAVAMMSVMVACRMV 770
                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Meoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              124 cttctgggtcccgtcctccaccttccccaaatgggtgaccaagacggaaaggggagaca 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          769 MMRSAVGAGMCAGACARAMAAMAMAMAAMRAAAVRASAAAAASRARARARAAGAGARAMM 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 gcccttgagatcctagacctgtggaaggccatcgatgggctcccctactcccacctcca 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         709 AAGARASARAGMMCAGMSRCAVACAGMSAVCAGAAVCMMGMCCRCSAVCVCCRSCCMSAC 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           244 cagccctccaagaggaatgtgatggagacgtttgccaaaccagagattggaggtaaagcc 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          649 GVGVRGSAGAGRAGACRARCGAGGRCCRSAVSAAMAVAAMMARAGCCGAGCACAMGCASA 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.8%; Score 41.6; DB 13; Length 919;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        385 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 23.0%; Pred. No. 5.4;
Matches 75; Conservative 105; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        177 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-98'
/clone="BACR14J09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="end : T7"
                                                                                                                                                                                                                                      Drosophila melanogaster
                                                                                                                                                                                          AL065856.1 GI:4944824
122 accttctgggtcccgt 137
                                338 ACCITCIGATGATCGT 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       77 c
                                                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                       fruit fly.
                                                                                                                                                                                                                                                                                                                      Genoscobe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                           DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                             CNS006S5/c
                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                  JOURNAL
                                                                                                                                                                                                         KEYWORDS
                                                                                                                                                                                       VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                    COMMENT
                                                                             RESULT
                                                                                                              LOCUS
Qγ
                            qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           qq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             δλ
```

ö

```
W83304 629 bp mRNA EST 12-SEP-1996 mf24d03.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA mf24d03.rl Soares mouse embryo NbME13.5 14.5 Mus musculus CDNA clone IMAGE:405989 5' similar to gb:M77140 GALANIN PRECURSOR (HUMAN); gb:L38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                 Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 629)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             188 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 56.79
Matches 76; Conservative
                                                                                                                                                               W83304.1 GI:1540498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           .629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGI:249757
                                                                                                                                                       W83304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                            DEFINITION
                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                     JOURNAL
                                                                                                                                                                                                                                                                                                   REFERENCE
                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURES
                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                  RESULT
                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           음
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ά
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/Darley/ To order a clone see http://www.genome.clemson.edu/orders" 206 c 365 g 202 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu. Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                   HVSMEf0004K09f Hordeum vulgare seedling root EST library HVCDNA0007 (eticlated and unstressed) Hordeum vulgare cDNA clone HVSMEf0004K09f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Development of a genetically and physically anchored EST resource for barley genomics Unpublished (2000) on Nov 16, 2000 this sequence version replaced gi:11183760.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 ctccagcatcggcacctgcccaccggggacgaggggggctggaccctcaatagtgctggct 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Hordeum vulgare seedling root EST library
HvCDNANAONO" (etiolated and unstressed)"
/tissue_type="Seedling root"
/lab_host="TJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 tggctcctccctccgtcccctggtcctcctcgtcctcttgctgagcctggcagaga 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
9.8%; Score 41.6; DB 11; Length 999;
Best Local Similarity 56.6%; Pred. No. 5.5;
Matches 77; Conservative 0; Mismatches 59; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clemson University Genomics Institute
Clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:4513"
/clone="HVSMEf0004K09f"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: rwing@clemson.edu
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 491.
Location/Qualifiers
                                                                                                                                                                                                             mRNA
                                                                   364 ttagaggatctgggcatgctcagcat 389
                                                                                                         529 AAGRAGARAAMRMRCWCACGCGASRK 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /cultivar="Morex"
                                                                                                                                                                                                                                                                                                                BF254655.2 GI:13117270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 ACCTTCTGATGATGT 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             122 accttctgggtcccgt 137
                                                                                                                                                                                                                 dq 666
                                                                                                                                                                                                                                                                                                   BF254655
                                                                                                                                                                                                                                                                                                                                                                barley.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                               RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                   ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                  BF254655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMENT
                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    òγ
```

```
Agrae, M. Hiller, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylle, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R. The WashU-HHM Mouse EST Project
Unpublished (1996)

N. Sep 12, 1996 this sequence version replaced gi:1394257.
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 140 ATGGCCAGAGGATGCGTTATCCTGCTAGGCTGGCTCGTTGTGACCCTGTCAGCC 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 atggetectecetecgtececetggtectectectegtectettgetgageetggeagag 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 41.2; DB 11; Length 629; 56.7%; Pred. No. 6.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="!MAGE:405989"
/clone="lMAGE:405989"
/clone=lib="Sqares mouse embryo NDMEl3.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: -28M13 rev2 from Amersham Seq primer: -28M13 requence stop: 440. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /sex="unknown
```

```
Search completed: March 2, 2002, 23:27:36 Job time: 10555 sec
                                                                                                                                       á
                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                δλ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pT713D-Pac (Pharmacia) with a modified Polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5, TT and the another of mRNA from 2: 13.5dpc and 2: 14.5dpc amburts of mRNA from 2: 13.5dpc and 2: 14.5dpc amburts of mRNA from 2: 13.5dpc and 2: State Univ. from 2: 13.6dpc amburts of mRNA from 2: 13.5dpc and 2: State Univ. from 2: 13.6dpc and 2: State Univ. from 2: State Univ. from 2: State Univ. from 3: 
                                                                                                                                                                                                                                                                                                                                                            W75493 642 bp mRNA EST 20-JUN-1996 me55bl2.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:391391 5' similar to 9b:M77140 GALANIN PRECURSOR (HUMAN )... 9b:L38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Maria, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Gelsel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 642)
200 ACTCTGGGACTTGGGATGCCTGCAAAGGAGAAGAGGTTGGACCCTGAACAGGGCTGGC 259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. MGI:24323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washu-HMI Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
9.7%; Score 41.2; DB 11; Length 642;
Best Local Similarity 56.7%; Pred. No. 6.2;
Matches 76; Conservative 0; Mismatches 58; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The Washu-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: mouseest@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 342.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:10090"
/clone="IMAGE:391391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     177 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.Fatima Bonaldo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex="unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W75493.1 GI:1385709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seq primer: ETPrimer
                                                                                    121 taccttctgggtcc 134
                                                                                                                               260 TACCTTCTGGGCCC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144
                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            source
                                                                                                                                                                                                                                                                                   RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMMENT
QQ
                                                                                δ
```

. 0

0; Gaps

58; Indels

1 atggctcctccctccgtcccctggtcctcctcctcgtccttgctgagcctggcagag 60

ò

```
61 actecageatecgeaectgeecaceggggaegaggaggetggaeceteaatagtgetgge 120
                                                   190 ACTCTGGGACTTGGGATGCCTGCAAAGGAAGGAGGTTGGACCCTGAACAGCGCTGGC 249
                                                                                                       121 taccttctgggtcc 134
                                                                                                                            250 TACCTTCTGGGCCC 263
```

```
Align seg 1/1 to: AQ549952 from: 1 to: 565
276.62
452.56
214.58
225.42
308.20
                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="GDB.7660399"
/db_xref="taxon:9606"
/clone="RPCI-11-418L8"
/clone_1lb="RPCI-11"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 142 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 C
 87.00
87.00
86.50
86.50
86.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5.132
                                                                                                                                                                                                                                                                                                                                                                          1. .565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             272.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-689-911-2 x AQ549952
                                                                                                                                                                                                                                                                                                                                                             Class: BAC ends
                                                      seq_name: gb_gss:AQ549952
                                                                                                                                                                                                          Map Building
                                                                       seq_documentation_block:
Locus
                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
                                                                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
 gb_est2:BF120807
gb_est2:BF861375
gb_est2:BG847573
gb_est2:BG676930
                                     gb_est2:BG683978
                                                                                        DEFINITION
                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BASE COUNT
                                                                                                           ACCESSION
                                                                                                                                                                       REFERENCE
                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                   JOURNAL
                                                                                                                    VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                 TITLE
                                                                                                                                      SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | BG717112 | BG89639F1 NIH_MGC_9 | BE688147 CM4-UT0008-050800-257- | BG770910 602670809F1 NIH_MGC_9 | BE973551 601680914F1 NIH_MGC_8 | BE197037 602756815F1 NIH_MGC_8 | AL258847 RPCI-23-2505.7.1 RPCI-1 AL236911 Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                           AL856408 AL556408 LTI NFL006 PI
AL556408 AL556408 LTI NFL006 PI
BL55627 602976496F1 NIH_MGC_1
BF551196 UT R-CO-hw-a 05-0-UI:
W75493 me55b12.r1 Soares mouse
AL556409 AL556409 LTI NFL006_PI
AL26589 PTELTAGOD INTOVITIGIS
AL8385770 mg99912.x1 Soares mouse
BF233017 602023543F1 NCI_CGAP_
                                                                                                                                                                                                                                                                                                AQ743759 HS_5501_A1_C03_T7A RPC
BF940993 hu62h04 xxl NCI_CGAP_Br
AX1009667 AJ009667 Homo sapiens
BEIL1677 UI-R-BJ1-avv-e-07-0-UI
BG244340 602356053F1 NCI_CGAP_
                                                                   ! Documentation
                                       About: Results were produced by the GenCore software, version 4.5, copyright (c) 1993-2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                        8804
11246
11246
11246
11246
11246
11244
11002
1232
1232
1232
1311
13157
                                                                                                                                                                                                                                                                                          EScore Len
4.6e-15 56
4.6e-13 46
2.5e-09 30
       out_format : pfs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      143.35
149.86
192.65
134.81
155.92
226.12
                                                                                                                                                                                                                                                                                                                                     5.09
5.09
7.744
14.44
14.44
118.81
118.81
118.81
118.81
118.81
113.90
10.09
10.09
10.09
113.09
113.09
110.09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  136.24
140.30
137.17
133.82
138.85
138.50
136.55
138.50
138.50
138.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
12
12
                                                                                                                                                                                                                                                                                            ZScore
435.05
398.98
331.97
166.91
164.20
164.20
                                                                                                                                                                                                                                                                                                                                                                                                                                                             10
88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
07
40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        43
                                                                                                                                                                                                                                                                                                                                                                                        949
949
97
97
97
       OM of: US-09-689-911-2 to: EST:*
                                                                                                                                                                                                                                                                                                    87.50
87.50
87.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            000
                                                                                                                                                                                                                                                Search time (sec): 1496.850000
                                                                                                                                                                                                              Query length: 141
Database: EST:*
Database sequences: 11351937
Database length: 10779219855
                        Date: Mar 3, 2002 12:21 AM
                                                                                                                                                                                            Search information block:
                                                                                                                                                                                                     Query: US-09-689-911-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est1:BE789912
gb_est1:A1188184
gb_est2:BI338510
gb_est2:BF679000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gb_est1:BE408867
gb_est2:BF966935
gb_est2:BF150728
gb_est1:BE614850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gb_est2:BG717310
gb_est1:BE698147
gb_est2:BG707910
                                                                                                                                                                                                                                                                                                                                                                                                  gb_gss:CNS03WDO
gb_est1:A1385770
gb_est2:BF233017
                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_est1:BE111677
gb_est2:BG244340
gb_est2:T03476
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gb_gs:CNS03WIC
gb_est1:BE788284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est2:BG701112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gb_est2:BE973551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gb_est2:BI197037
                                                                                                                                                                                                                                                                                                                                       gb_est2:W83304
gb_est1:A1894042
gb_est1:AL556408
                                                                                                                                                                                                                                                                                                                                                                gb_est2:BI255627
gb_est2:BF551196
gb_est2:W75493
                                                                                                                                                                                                                                                                                                                                                                                                                           gb_gss:AQ743759
gb_est2:BF940993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gb_est1:A1178481
                                                                                                                                                                                                                                                                                                                      gb_est1:AW436648
                                                                                                                                                                                                                                                                                                     gb_gss:AQ549952
gb_est1:AW416677
                                                                                                                                                                                                                                                                                                                               gb_est1:AW141500
                                                                                                                                                                                                                                                                                                                                                                                          gb_estl:AL556409
                                                                                                                                                                                                                                                                                                                                                                                                                                              gb_est1:AJ009667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gb_gss:A2558872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gb_gss:AZ099906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gb_gss:CNS03BSM
                                                                                                                                                                                                                                                                                     score_list:
                                                                    Command
```

```
1 BF120807 601757407F1 NCI_CG
                        | BFB61375 963022F05.x1 C. r
| BGB47573 1024018A10.x1 C. r
| BG676930 602653544F1 NOI_CG
| BG683978 602651479F1 NIH_MG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: bbe@tigr.org

Elibrary availability, please contact Pieter de Jong

library availability, please contact Pieter de Jong

(pieter@dejong.med.buffalo.edu). Clones may be purchased from

Resources (http://bacpac.med.buffalo.edu/ordering) or from

Research Genet cs (info@tesgen.com). BAC end search page:

http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                      AQ549952 565 bp DNA GSS 28-MAY-1999 RPCI-11-418L8, DNA sequence.
AQ549952 GI:4909129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 565)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zhao, S., Adams, M.D., Nierman, W., Malek, J., de Jong, P. and Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
RPCIII Human Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 IleAspGlyLeuProTyrSerHisProProGlnProSerLysArgAsnVa 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Outbullshed (1997)
Other_GSSs: RPCI-11-418L8.TV
Other_HSSs: RPCI-11-418L8.TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length: 55
Gaps: 0
Percent Identity: 90.909
```

```
source
                                                                                                                                                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASE COUNT
                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                                                                                                                                    VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMMENT
                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                     Takrenkrug's.C., Freking'B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Fax: 402 762 4366
Fax: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 465)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pcMV SPORT6; Site_1: Xbal; Site_2: Xhol; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                09-JUL-2000
52226 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81 ACTGTCCTTGTTGTTGTTGTTC...CTGCTCAGCCTGATGGAGTC 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 ServalProLeuValLeuLeuValLeuLeuLeuSerLeuAlaGluTh 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 1
Percent Identity: 73.529
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AW416677 from: 1 to: 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BACKWARD: GTTTTCCCAGTCACGACG
Plate: 24 row: B column: 13
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                            AW416677.1 GI:6944559
                                                                                                                                                                                                        465 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               248.50
4.212
86.765
                                                                           122 LeuGluAspLeuGly 126
                                                                                                            522 TTACAGGGTAAAGGA 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-689-911-2 x AW416677
                                                                                                                                                     seq_name: gb_est1:AW416677
                                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                       Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ď
                                                                                                                                                                                                            AW416677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                               AW416677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores:
                                                                                                                                                                                                                                                                                                         pig.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                         DEFINITION
                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                             ACCESSION
                                                                                                                                                                                                                                                            VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                   SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGIN
```

```
Single pass sequencing. Bases called and trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 20 and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. ( bases 1 to 304)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreld, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Design and use of two pooled tissue normalized cDNA libraries for instance of two pooled tissue normalized cDNA libraries for instance (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
De Dox 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pcwv sports; Site_1: xbal; Site_2: Xhol; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta."
                                                                                                                                                                                                                                                                                                                                             09-JUL-2000
                                                                                   77047 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
AW436648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Identity: 70.690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to: AW436648 from: 1 to: 304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="MARC 2PIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGCCC
Plate: 32 row: F column: 8
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="pooled"
/lab_host="DH108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                       AW436648.1 GI:6971954
                                                                                                                                                                                                                                                                                                                                        304 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 204.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-689-911-2 x AW436648
                                                                                                                                                                                                                                                                       seq_name: gb_est1:AW436648
                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   57 a
                                                                                                                                                                                                                                                                                                                                        AW436648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                          278 CATT 281
                                                                                                                                                                              71 aile 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
```

```
AW141500 498 bp mRNA EST 30-OCT-1999 EST2291550 Normalized rat embryo, Bento Soares Rattus sp. cDNA clone RGIBW81 5' end similar to galanin, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lee, N.H., Glodek, A., Chandra, I., Mason, T.M., Quackenbush, J., Kerlavage, A.R. and Adams, M.D. Rat Genome Project: Generation of a Rat EST (REST) Catalog & Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Normalized rat embryo, Bento Soares"
/clone_lib="Normalized rat embryo, Bento Soares"
/dev_stage="embryo 8, 12, 18 dpc"
/note="Vector: pT/T3Pac; Site_1: EcoRI; Site_2: NotI"
/note="Vector: pT/T3Pac; Site_1 to thers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-3529
Fox: (301)-838-0208
Email: nhlee@tigr.org
For clone availability, additional sequence and expression
Information related to this EST please check the TIGR Rat Gene
Information. Telated to this Conference of the Conference of the ATCC (http://www.atcc.org/atcc.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       195 CCTGTCAGCCACTCTGGGGCTCGGGATGCCAACAAAGGAGAAGAGAGGGCT 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MetAlaProProSerValProLeuValLeuLeuLeuValLeuLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
38 erAlaGlyTyrLeuLeuGlyProValLeuHisLeuProGlnMetGlyAsp 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 41.429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AW141500 from: 1 to: 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Rattus sp."
/db_xref="taxon:10118"
/clone="RGIBW81"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                              279 GGAGGCGGAAGGGGAAGACAGCC 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seg primer: M13 Reverse.
                                                                                                                                                                                       55 GlnAspGlyLysArgGluThrAla 62
                                                                                                                                                                                                                                                                                                                                                                                                               AW141500
AW141500.1 GI:6161294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (bases 1 to 498)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            104.50
2.322
64:286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-689-911-2 x AW141500
                                                                                                                                                                                                                                                                           seq_name: gb_est1:AW141500
                                                                                                                                                                                                                                                                                                                          sed_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     source
                                                                                                                                                                                                                                                                                                                                                                       DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                    ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOURCE
```

```
DEFINITION mf24603.rl Soares mouse employ obbel3.5 14.5 Mus musculus cDNA clone IMAGE:405989 5' similar to gb:M77140 GALANIN PRECURSOR (HUMAN ); gb:L38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Marra, M. Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Marra, M., Hillier, L., Allen, M., Le, M., Martin, J., Morris, M., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: mouseest@watson.wustl.edu
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R. The Wash of the 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="c57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:405989"
/clone_lib="Soares mouse embryo NbME13.5 14.5"
                                       295 CACAGATCATTAGCGACAAGCATGGCCTCACAGGCAAGAGGGAGTTACC 344
34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48
                                                                                                                                                                 49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
/dev.stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 440. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                137 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       166 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /sex="unknown"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          629 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W83304.1 GI:1540498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est2:W83304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 a
                                                                                                                                                                                                                                                                                                                                                                                                                                  345 ACTGGAAGTG 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGI:249757
                                                                                                                                                                                                                                                                                                                                                   62 aLeuGluIle 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W83304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
```

ORIGIN

```
alignment_scores:
                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACCESSION
VERSION
                                                                     FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCUS AI894042 679 bp mRNA EST 15-MAR-2000
DEFINITION mg89912.yl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMACE:440230 5' similar to 9b:M77140 GALANIN PRECURSOR (HUMAN ); 9b:L38580 Mus musculus galanin gene (MOUSE); mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enkaryota, Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Ritter Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a REEGQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                                                 290 CACAGATCATTTAGCGACAAGCATGGCCTCACAGGCAAGAGGGAGTTACA 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               111111::: :::
340 ACTGGAGGTGGAGGAGGAGGAGGTGTTGATGTGCCCCTG.... 385
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MetAlaProProSerValProLeuValLeuLeuLeuValLeuLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                             17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            62 aLeuGlulleLeuAspLeuTrpLysAlalleAspGlyLeuProTyrSerH 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79 isProProGlnProSerLysArgAsnValMetGluThrPheAlaLysPro 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96 GluileGlyGlyLysAlaArgLySHisArgArgGluThrProThrGly 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   434 CACCITAAAGGCCGGGGCCCTCGACAGCCTGCCTGGCATCCCCTTGGC 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
Other ESTs: mg89g12.x1
Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                             Percent Identity: 31,034
                                  Length:
                                                                                                                                                                                     Align 2eg 1/1 to: W83304 from: 1 to: 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AI894042.1 GI:5599944
                                                 1.560
                           Quality: 104.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  314 286 1800
314 286 1810
                                                                                                                  alignment_block:
US-09-689-911-2 x W83304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: gb_est1:AI894042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
LOCUS AI894042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       house mouse.
                                                                Percent Similarity:
                                                 Ratio:
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
```

```
T 3'], on equal amounts of mRNA from 2 13.5dpc and 2 14.5dpc embryos [total RNA provided by Minoru Ko, Wayne State Univ., from 2 ]; double-stranded cDNA was ligated to cloned into the Not I and Bco RI sites of the modified pT/73 vector. Library went through one round of M. Fatima Bonaldo. " and was constructed by Bento Soares and M. Fatima Bonaldo." 156 t 1 others
                                                                                                                                                                                                                                                                                                                            AL556408 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK004YA08 3 AL556408.1 GI:12899056
                                                                                                                                                                                                                       /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 CCTGTCAGCCACTCTGGGACTTGGGATGCCTGCAAAGGAGAAGAGAGGTT 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 CACAGATCATTTAGCGACAAGCATGGCCTCACAGGCAAGAGGGAGTTACA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |||||||::: :::||||
330 ACTGGAGGTGGAGGAAAGGAGCAGGAAGTGTTGATGTGCCCCTG.... 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MetAlaProProSerValProLeuValLeuLeuLeuValLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 aLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProTyrSerH 79
                                                                                                                                                                                                                                                                                    /dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps: 3
Percent Identity: 35.789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     376 ..CCTGAGAGCATTGTCGCACTATAATGGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79 isProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AI894042 from: 1 to: 679
                                                                                                                                /organism="Mus musculus"
                                                        High quality sequence stop: 402.
                                                                                                                                                                        /db_xref="taxon:10090"
                                                                                                                                                                                                    /clone="IMAGE:440230
                                                                                                                                                                                                                                                                 /tissue_type="embryo
              MGI:265566
Seq primer: -40RP from Gibco
                                                                                                                                                   /strain="C57BL/6J
                                                                                                                                                                                                                                                 /sex="unknown
orientation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio: 1.833
Percent Similarity: 60.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 104.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-689-911-2 x AI894042
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: gb_est1:AL556408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
```

```
source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASE COUNT
                                                                   ORGANISM
                                                                                                                                     AUTHORS
                                                                                                                                                                        JOURNAL
ACCESSION
                                                                                                                      REFERENCE
                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                  KEYWORDS
                                                                                                                                                     TITLE
                                                                                                                                                                                        COMMENT
                  VERSION
                                               SOURCE
                                                                                                                                                                                                                                                                            LOCUS B1255627 760 bp mRNA EST 17-JUL-2001 DEFINITION 602976496F1 NIH_MGC_12 Homo sapiens CDNA clone IMAGE:5115887 5',
                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                    Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
__Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              334 GACAAGAATGGCCTCACCAGTAAGCGGGAGCTGCGGCCCGAA..... 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  292 ......GATGACATGAAACCAGGAAGCTTIGACAGGTCCATTT 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 crecrecrecrecrerecreses 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 ......ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 laglyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 AspGlnAspGly......LysArgGluThrAlaLeuGluIleLeuAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 pleuTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10 LeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Align seg 1/1 to reverse of: AL556408 from: 1 to: 727
                                                                                    Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 104.50 Length: 91 Ratio: 2.010 Gaps: 5 Percent Similarity: 57.143 Percent Identity: 42.857
                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255 CTGAAAACAATATCATGCGCACA 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         84 erLysArgAsnValMetGluThr 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-689-911-2 x AL556408/rev
                                                                            (bases 1 to 727)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seg_name: gb_est2:BI255627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg_documentation_block:
                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BASE COUNT
                                ORGANISM
                                                                                                                 TITLE
JOURNAL
                                                                                                  AUTHORS
                                                                                  REFERENCE
KEYWORDS
                                                                                                                                                                                                                         FEATURES
                                                                                                                                                    COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGIN
```

```
/note-"Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
                                                                                                      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bummalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 760)
NIH-WGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                    Email: cgapbs-rémail.nih.gov
Tissue procurement. Troc
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.ocolumn: 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 crecircrecerecerecreseseseseseses 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       280 CGGGCTACCTGCTGGGCCCACATGCCGTTGGCAACCACAGGTCATTCAGC 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     330 GACAAGAATGGCCTCACCAGCAAGCGGGAGCTGCGGCCGAAGATGACATG 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   67 pLeuTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39 laglyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 AspGlnAspGly......LysArgGluThrAlaLeuGluIleLeuAs 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 LeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla.. 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 91
Gaps: 6
Percent Identity: 41.758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: BI255627 from: 1 to: 760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
                                                                                                                                                                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:9606"
/clone="IMAGE:5115887"
/clone_lib="NIH_MGC_12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High quality sequence stop: 645.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      202 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                409 GTGAAAACAATATCATGCGCACA 431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   84 erLysArgAsnValMetGluThr 91
                                      BI255627.1 GI:14809207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           253 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity: 59.341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103.50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .760
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_block:
US-09-689-911-2 x BI255627
mRNA sequence.
BI255627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           172 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                      human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
```

Percent Identity: 37.000

to: 423

```
157 ccrercaeceacregegecregegargecaacaaaggagaaragagger 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                   251 GACAACCACAGATCATTTATCGACAAGCATGGC...CTCACAGGCAAGAG 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MetAlaProProSerValProLeuValLeuLeuValLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   348 CCCTGCCTGAGAGCAAT.....ATCGTCGGCACTATAATGGAG 385
                                                                                                                                                                                                                                                                                                                  17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                                                                                                                                                         34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyProValLeuHis..... 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 .........LeuProGlnMetGlyAspGlnAspGlyLysAr 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 gGluThrAlaLeuGluIleLeuAsp.....LeuTrpLysAlaIleAspG 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           74 lyLeuProTyrSerHisProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                          Align seg 1/1 to: BF551196 from: 1
                         Percent Similarity: 55.000
                                                                         alignment_block:
US-09-689-911-2 x BF551196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est2:W75493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 // Anote-Tubector: pTT3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-CO library is a subtracted library defrom the UI-R-CO and UI-R-E1 libraries. The UI-R-A1 library consisted of a mixture of individually tagged normalized libraries constructed from at placente, adult lung, brain, library consisted of a mixture of individually tagged normalized libraries constructed from B, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dr track which allows identification of the library of origin of a clone constructed as follows: PCR amplified cDNA inserts from a been derived was used as a fullors in a hybridization with the pooled UI-R-A1 and UI-R-E1 library in a hybridization with single-stranded circles. The remaining single-stranded circles (subtracted library in the form of single-stranded circles. The remaining single-stranded circles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: msoares@blue.weeg.uiowa.edu

CDNA Library Preparation: M.B. Soares Lab Clone distribution:

clones will be available through Research Genetics (www.resgen.com)

This clone is also available through the I.M.A.G.E. Consortium at

LLNL (info@image.llnl.gov). IMAGE ID= 1773887

Seq primer: M13 Forward.
                                                                                                                                                                                                                                                                                           Eukaryota; Mētazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                 1 (bases 1 to 423)
Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              library. This procedure has been pressure (Bonaldo, Lennon and Soares, Genome Research 6: 791-806,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
                                                                                               12-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DHIOB bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described
                                                                      BF551196 423 bp mRNA BST 12-DEC-2000C UI-R-CO-hw-a-05-0-UI.rl UI-R-CO Rattus norvegicus cDNA clone UI-R-CO-hw-a-05-0-UI 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain-"Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-CO-hw-a-05-0-UI"
/clone_lib="UI-R-CO"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Rattus norvegicus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     82 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rès. 6 (9), 791-806 (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 9
                                                                                                                                                                                   BF551196.1 GI:11660926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Iowa
                                                                                                                                                                                                                                                                  Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             128 c
seq_name: gb_est2:BF551196
                                               Norway rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97044477
                                                                                                                                                                                                                                                                                                                                                      Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                               DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Source
                                                                                                                                                                                                                                                               ORGANISM
                                                                                                                                                    ACCESSION
```

FEATURES

MEDLINE COMMENT

JOURNAL

REFERENCE AUTHORS

TITLE

KEYWORDS

SOURCE

VERSION

```
W75493 642 bp mRNA EST 20-JUN-1996 me55bl2.rl Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:991391 5' similar to 9b:M77140 GALANIN PRECURSOR (HUMAN); gp:L38580 Mus musculus galanin gene (MOUSE);, mRNA sequence.
                                                                                                                                                                                                                                                                                 Mammalia; Butheria; Rodentia; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 642)
Marra M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Mark Mydouse EST Project
WashU-HHMI Mouse EST Project
WashIngton University School of MedicineP
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fax: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Waterston, R.
The WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             High quality sequence stop: 342.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:10090"
/clone="IMAGE:391391"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /sex="unknown'
                                                                                                                                                                W75493.1 GI:1385709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: ETPrimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1996)
```

Gaps: Length:

Quality: 100.50 Ratio: 1.827

BASE COUNT

ORIGIN

us-09-689-911-2.rst

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

( bases 1 to 804)

Li,W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AL556409 LTI_NFL006_PL2 Homo sapiens cDNA clone CSODK004YA08 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        280 CACAGATCATTTAGCGACAAGCATGGCCTCACAGGGAAGAGGGGAGTTACA 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 GGACCCTGAACAGCGCTGGCTACCTTCTGGGCCCACATGCCATTGACAAC 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                330 ACTGGAGGTGGAGGAAAGGAGCCAGGAAGTGTTGATGTGCCCCTG.... 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34 rpThrLeuAsnSerAlaGlyTyrLeuLeuGlyPro.....ValLeuHis 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49 LeuProGlnMetGlyAspGln.....AspGlyLySArgGluThrAl 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MetAlaProProSerValProLeuValLeuLeuLeuValLeuLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62 aLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProTyrSerH 79
/tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                               99.50 Length: 95
1.777 Gaps: 3
58.947 Percent Identity: 34.737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
                                                                                                                                                                                                                                                                       142 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       376 ..CCTGAGAGCAACATTGTCCGCACTATAATGGAG 408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    79 isProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
                                                                                                                                                                                                                                        normalication M.Fatima Bonaldo. '
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AL556409.1 GI:12899058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prime, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  804 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: W75493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: gb_est1:AL556409
                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-689-911-2 x W75493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
JS AL556409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numan.
                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                              ORIGIN
```

```
/organism="Homo sapiens"
/organism="Homo sapiens"
/db.xref="CSODKO04XA08"
/clone="CSODKO04XA08"
/clone=lib="LTI_NELO06_PL2"
/tissue_type="placenta"
/tissue_type="placenta"
/note="Vector: pCNVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCWVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Library was constructed by
Life Technologies. Contact: Library was contact. Library was constructed by
Life Technologies. Contact: Library was contact. Library was co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CNSO3WDO 745 bp DNA GSS 18-MAY-2000 Tetraodon nigroviridis genome survey sequence T7 end of clone 064A13 of library G from Tetraodon nigroviridis, genomic survey
434 .....GATGACATGAAACCAGGAAGCTTTGACAGGTCCATAC 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             342 CGGGCTACCTGCTGGGCCCATGCCGTTGGCAACCACAGGTCATTCAGC 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 245 CICCIGCICGCCCCCCCCCCCCCCCCCTICTGCCCCCC 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    295 GCTCTGGTCGCCGGCCAAGGAAAACGA...GGCTGGACCCTGAACAGG 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 .....ProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 laGlyTyrLeuLeuGlyPro.....ValLeuHisLeuProGlnMetGly 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 pLeuTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 LeuLeuLeuValLeuLeuLeuSerLeuAlaGluThrProAlaSerAla..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 54 AspGlnAspGly......LysArgGluThrAlaLeuGluIleLeuAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 91
Gaps: 5
Percent Identity: 41.758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AL556409 from: 1 to: 804
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSS; genome survey sequence. Tetraodon nigroviridis. Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tetraodontidae; Tetraodon.
1 (bases 1 to 745)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           471 CTGAAAACAATATCATGCGCACA 493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence.
AL263589
AL263589.1 GI:7985255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          84 erLysArgAsnValMetGluThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99.50
1.951
56.044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-689-911-2 x AL556409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_gss:CNS03WDO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KEYWORDS
                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
```

```
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and Weissenbach, J.
                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
                                                                                                                                                                                                                                                   Human gene number estimate provided by genome wide analysis using
Tetraodon nigroviridis DNA sequence
                                                                             Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="G"
/rone="Genoscope sequence ID : COBGO64AA07LP1-end : T7"
| 185 c 228 g 157 t 3 others
                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306 ccrccrrccrcccrccaggccagcrgcrccaaccrgrcrgcgrarcrgc 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          206 TGCAGCCA.......GGCCCTGTGCGCCTTCCACGGCCGCTG 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             85 ysArgAsnValMetGluThrPheAlaLysProGluIleGlyGlyLysAla 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   19 aGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyTrpThrL 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36 euAsnSerAlaGlyTyrLeuLeuGlyProVal...LeuHisLeuProGln 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 ProProSerValProLeuValLeuLeuLeuValLeuLeuLeuSerLeuAl 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             68 uTrpLysAlalleAspGlyLeuProTyrSerHisProProGlnProSerL 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52 MetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLe 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              113 ATCAGCAG.......CCGCAGCGGGAGGCCGGAGGTCAGCGG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         171 CCAGCGCAGGAACCCGGACAGCGA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Align seg 1/1 to reverse of: CNS03WDO from: 1 to: 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 5
Percent Identity: 31.858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="064A13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               102 ArgLysHisArg...ArgGluThrProThrGlyGluGly 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 AGACCTGGGCGAGGCCGACAAGTCCAGGCTGGGCGCGGA 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                      (bases 1 to 745)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-689-911-2 x CNS03WDO/rev
                                                                                                                                                                                                                                                                                                                           (bases 1 to 745)
                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.750
49.558
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               98.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: gb_est1:AI385770
                                                                                                                         Unpublished
                                                                                                                                                                                                                                                                                                    Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                           3 (bases Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ø
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
AUTHORS
                                                                                                                         JOURNAL
                                                                                                                                                REFERENCE
                                                                                                                                                                        AUTHORS
                                                                                                                                                                                                                                                                                               JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                            JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                        TITLE
                                                                                                                                                                                                                                                TITLE
                                                                                                                                                                                                                                                                                                                                                                       TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGIN
```

```
/ACCE="Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Ist strand cDNA was primed with a Not I · oligo(dT) primer [5] variant with a Not I · oligo(dT) primer [5] variant with a Not I · oligo(dT) primer [5] variant with a Not I · oligo(dT) primer [5] variant va
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Manmalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 559)
Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,E., Swaller,T., Gibbons,M., Pepe,D., Harvey,N., Schurk,R., Ritter,Watterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
AL385770 559 bp mRNA EST 27-JAN-1999 mg89912.x1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:440230 3' similar to gb:L38580 Mus musculus galanin A1385770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This clone was previously sequenced on the 5' end only, this new
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: mouseest@watson.wustl.edu
This clone is available royalty free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
TEL: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Soares mouse embryo NbME13.5 14.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         559 Argecagageagegrarecraerassersescriers...srrsraac 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MetAlaProProSerValProLeuValLeuLeuLeuValLeuLeuSe 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Marra M/WashU-NCI Mouse EST Project 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="embryo"
/dev_stage="13.5-14.5dpc total fetus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to reverse of: A1385770 from: 1 to: 559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Percent Identity: 35.789
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               149 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              data is from the 3' end
High quality sequence stop: 433.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:440230"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           131 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /sex="unknown"
                                                                                                                                                                                                                                                                                          AI385770.1 GI:4199233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-689-911-2 x AI385770/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.50
1.773
57.895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .559
                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       source
                                                                                                             DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BASE COUNT
                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE
                                                                                                                                                                                                                                                                                      VERSION
KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMMENT
                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGIN
```

17 rLeuAlaGluThrProAlaSerAlaProAlaHisArgGlyArgGlyGlyT 34

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Musmmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 1246)

8 NIH-Mac http://mgc.nci.nlh.gov/

8 NIH-Mac http://mgc.nci.nlh.gov/

1 Unpublished (1999)

8 Ontact: Robert Strausberg, Ph.D.

8 Email: cgapbs-remail.nih.gov

7 Tissue Procurement: Jeffrey E. Green, M.D.

8 CDNA Library Preparation: Life Technologies, Inc.

9 CDNA Library Preparation: Life Technologies, Conscritum (LLNL)

9 DNA Sequencing by: Incyte Genomics, Inc.

10 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

11 (http://image.llh.gov)

12 Plate: LLAM9435 row: f column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          415 CACAGATCATTAGCGACAAGCATGGCCTCACAGGCAAGAGGGAGTTACA 366
                                                                                                                                                                                                      62 aLeuGluIleLeuAspLeuTrpLysAlaIleAspGlyLeuProTyrSerH 79
                                                                                                                               49 LeuProGlnMetGlyAspGln.....AspGlyLysArgGluThrAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Percent Identity: 23.164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from: 1 to: 1246
                                                                                                                                                                                                                                                                                                                     319 ..CCTGAGAGCAACATTGTCCGCACTATAATGGAG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   e: LLAM9435 row: f column: 11 quality sequence stop: 609.
                                                                                                                                                                                                                                                                                   79 isProProGlnProSerLysArgAsnValMetGlu 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="FVB/N"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF233017.1 GI:11142797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1.390 38.418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: BF233017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-189-911-2 x BF233017
                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                             seq_name: gb_est2:BF233017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE
AUTHORS
TITLE
JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOURCE
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

[ (pases 1 to 850)
Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999) 99380589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clones are derived from the human BAC library RPCI-11. For BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block: 850 bp DNA GSS 16-JUL-1999 LOCUS AQ743799 BSO PP Human Male BAC Library Homo sapiens DEFINITION HS_5501_A1_C03_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1077 Col=5 Row=E, DNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1006 ACACAAAGACCGACGCAACACAGAGGGCAGGGACAGAAAGCGGAGACAG 1055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      956 AGAGAAGAAGAAAAGAGGCAACGAGAAAGCAAGAACGAGGCAGGAACCC 1005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 ......ArgGluThrProThrGlyGluGlyGluGlnGln.....Gl 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....GlyLysAlaArgLysHisArg... 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             856 ACGAAAACCAACAACAACACGACGAACAAAAACAGACCAGACAAACAC 905
                                                                                                                                                                                                                                    706 GGAAGGGGACAGCGGCCTCAAAGGGGGGACTTGGGGCCCCAAGGAGACACCCA 755
                                                                                                                                                                                                                                                                                                                                    756 ACACGTGAAAGGCCTCATGTGCAGAAAGAAGCCGCGATAAACATCCACGC 805
                                                                                                                                                                                                                                                                                                                                                                                                                             806 CGTATTTTTTTTGCGTGCCTCCTATCACCACCTCTCAACACAA 855
                           83 oSerLysArgAsnValMetGluThrPheAlaLysProGluIleGly.... 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 rLeuLeuGlyProValLeuHisLeuProGlnMetGlyAspGlnAspGlyL 58
                                                                                                                                                                                         58 ysArgGluThrAlaLeuGluIleLeuAspLeu......68
25 AlaProAlaHisArgGlyArgGlyGlyTrpThrLeuAsnSerAlaGlyTy 41
                                                                                                                                                                                                                                                                                                                                                                                    69 .....TrpLysAlaIleAspGlyLeuProTyrSerHis.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mahairas GG, Wallace JC, Hood L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High Throughput Sequencing Center
University of Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     116 ySerGlyArgGlnSerLeuGluAspLeuGly 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÃQ743759
AQ743759.1 GI:5521281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: gb_gss:AQ743759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDI, INE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOURCE
```

```
/Organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="blate=1077 Col=5 Row=E"
/clone=1bla=RPDI-11 Human Male BAC Library"
/sex="male."
/nord="Vector: pas. Size | EcoRi; Site_1: EcoRi; Site_2: EcoRi;
Male blood DNA was isolated from one randomly chosen donor and partially digested with a combination of EcoRi and partially digested with a combination of EcoRi and pBACc3.6 vector at EcoRI sites.

244 c 419 g EcoRI sites.
library availability, please contact Pieter de Jong (pieterédejong med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@fresgen.com). BAC end Web Server: http://www.htsc.washington.edu
Plate: 1077 row: E column: 5
Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           395 CAGGGGGGGCCACCCACCAGCAGCAGGGA.......GGCCAGAGGC 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         525 ......GACGGACG......CCCCCGCGAGGGGCCG 549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  550 caccecaegegegegaac.....egc 569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99 GlyLysAlaArgLysHisArgArgGluThrProThrGly.GluGlyGluG 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19 AlaGluThrProAlaSerAlaPro.....AlaHisArgGl 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30 yArgGlyGlyTrpThrLeuAsnSerAlaGlyTyrLeuLeuGly..... 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45 ......ProValLeuHisLeuPro.....Gln 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      52 MetGlyAspGlnAspGlyLysArgGluThrAlaLeuGluIleLeuAspLe 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 uTrpLysAlaileAspGlyLeuProTyrSerHisProProGln..... 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         83 ..ProSerLysArgAsnValMetGluThrPheAlaLysProGluIleGly 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 9
Percent Identity: 32.520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 850
                                                                                                                                                                                High quality sequence stop: 850.
Location/Qualifiers
1.850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115 lnGlySerGlyArgGln 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality: 93.50
Ratio: 1.612
Percent Similarity: 47.154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      620 AGGGGGGGGGCCGCAG 636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align eg 1/1 to: AQ743759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-689-911-2 x AQ743759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                    source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BASE COUNT
                                                                                                                                                                                                          FEATURES
```